



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 12:47 PM UTC

PDB ID : 6XYW / pdb\_00006xyw  
EMDB ID : EMD-10654  
Title : Structure of the plant mitochondrial ribosome  
Authors : Soufari, H.; Waltz, F.; Bochler, A.; Giege, P.; Hashem, Y.  
Deposited on : 2020-01-31  
Resolution : 3.86 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

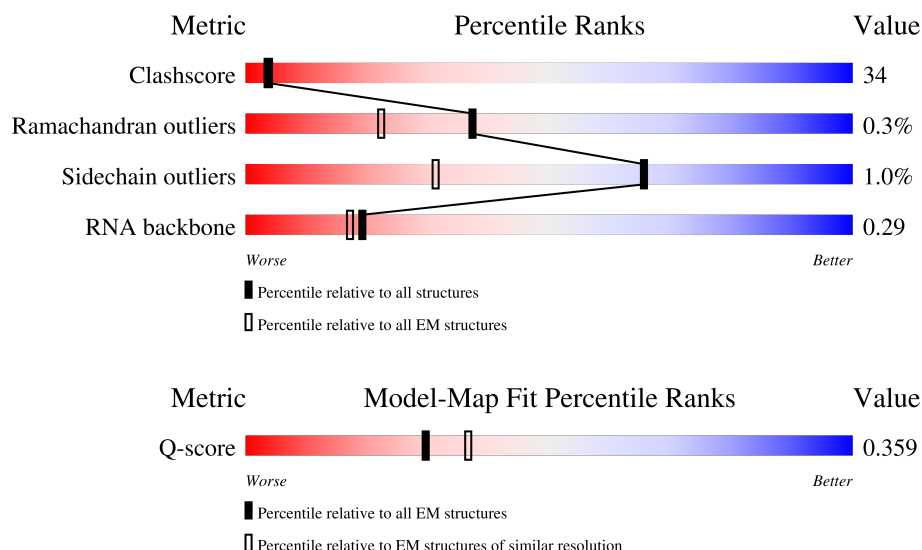
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.86 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



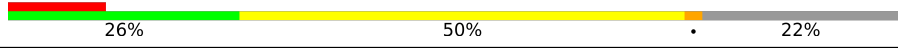
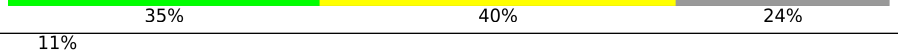
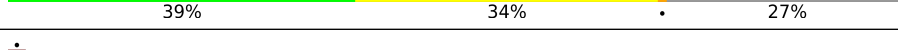
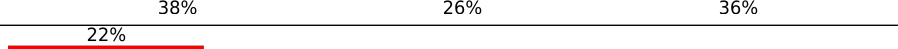
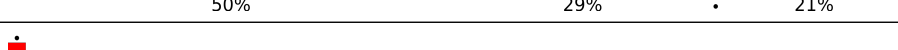
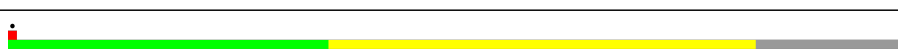
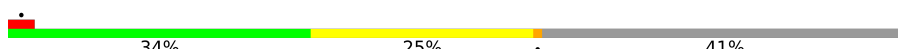
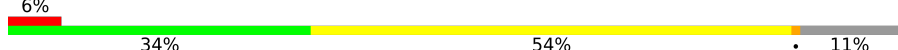
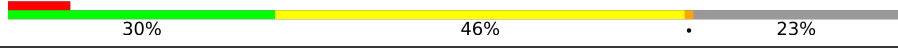
| Metric                | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore            | 229148                      | 23984                       | -                                                        |
| Ramachandran outliers | 224038                      | 23583                       | -                                                        |
| Sidechain outliers    | 223484                      | 23102                       | -                                                        |
| RNA backbone          | 8273                        | 3508                        | -                                                        |
| Q-score               | -                           | 25397                       | 8889 ( 3.36 - 4.35 )                                     |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1   | Aa    | 349    |                  |
| 2   | Ab    | 214    |                  |
| 3   | Ac    | 324    |                  |

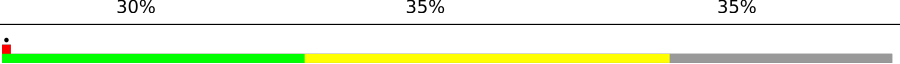
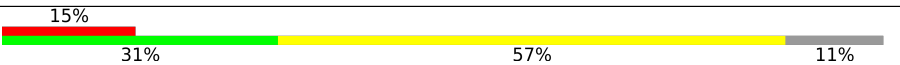
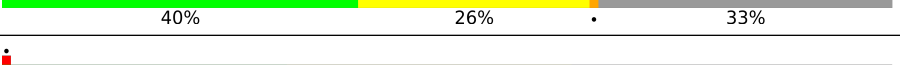
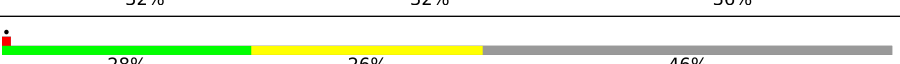
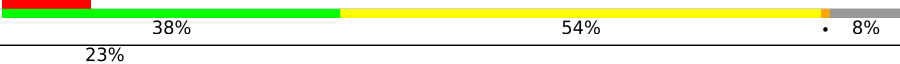
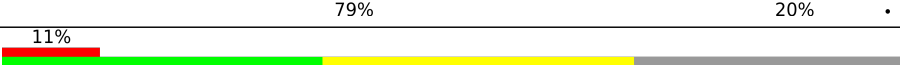
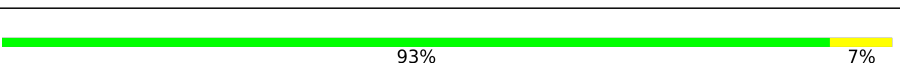
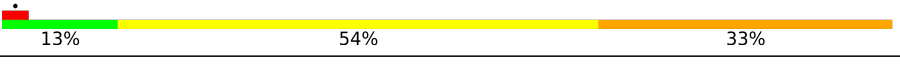
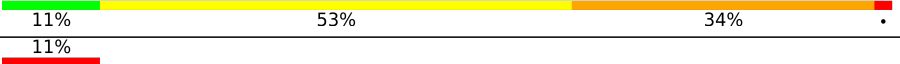
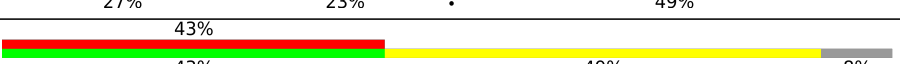
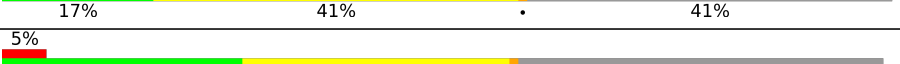
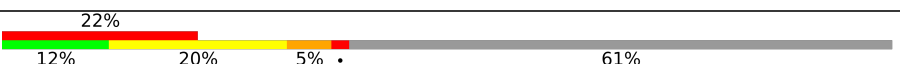
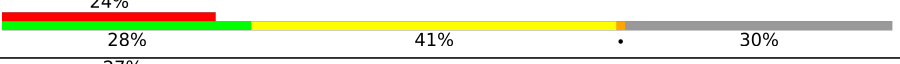
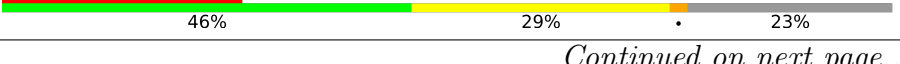
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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 4   | AD    | 173    |    |
| 5   | Ad    | 300    |    |
| 6   | Ae    | 185    |    |
| 7   | Af    | 102    |    |
| 8   | Ag    | 221    |    |
| 9   | Ai    | 155    |    |
| 10  | Aj    | 205    |    |
| 11  | Ak    | 173    |    |
| 12  | Al    | 281    |    |
| 13  | Am    | 179    |    |
| 14  | An    | 160    |    |
| 15  | Ao    | 114    |  |
| 16  | Ap    | 222    |  |
| 17  | Aq    | 126    |  |
| 18  | Ar    | 270    |  |
| 19  | As    | 269    |  |
| 20  | At    | 178    |  |
| 21  | Au    | 159    |  |
| 22  | Av    | 249    |  |
| 23  | Aw    | 154    |  |
| 24  | Ax    | 212    |  |
| 25  | Ay    | 144    |  |
| 26  | AA    | 76     |  |
| 27  | AB    | 134    |  |
| 28  | AC    | 58     |  |

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| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 29  | AE    | 103    |    |
| 30  | AF    | 250    |    |
| 31  | AG    | 94     |    |
| 32  | AH    | 146    |    |
| 33  | AI    | 233    |    |
| 34  | AJ    | 127    |    |
| 35  | AK    | 130    |    |
| 36  | AL    | 81     |    |
| 37  | AM    | 151    |    |
| 38  | AN    | 188    |   |
| 39  | AO    | 491    |  |
| 40  | AP    | 669    |  |
| 41  | AQ    | 521    |  |
| 42  | AR    | 29     |  |
| 43  | 1     | 2842   |  |
| 44  | 3     | 118    |  |
| 45  | Bb    | 556    |  |
| 46  | Bf    | 148    |  |
| 47  | Bh    | 430    |  |
| 48  | Bi    | 241    |  |
| 49  | Bl    | 154    |  |
| 50  | Bm    | 164    |  |
| 51  | Br    | 212    |  |
| 52  | Bw    | 480    |  |
| 53  | Bx    | 102    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 54  | Bz    | 419    |                  |
| 55  | BA    | 91     |                  |
| 56  | Bt    | 98     |                  |
| 57  | BG    | 576    |                  |
| 58  | BP    | 91     |                  |
| 59  | BF    | 123    |                  |
| 60  | Ba    | 219    |                  |
| 61  | Bc    | 362    |                  |
| 62  | Bd    | 515    |                  |
| 63  | Be    | 139    |                  |
| 64  | Bg    | 129    |                  |
| 65  | Bj    | 314    |                  |
| 66  | Bn    | 419    |                  |
| 67  | Bo    | 135    |                  |
| 68  | Bp    | 116    |                  |
| 69  | Bq    | 261    |                  |
| 70  | Bs    | 101    |                  |
| 71  | Bu    | 195    |                  |
| 72  | Bv    | 195    |                  |
| 73  | By    | 142    |                  |
| 74  | BB    | 137    |                  |
| 75  | BC    | 112    |                  |
| 76  | BD    | 420    |                  |
| 77  | BE    | 409    |                  |
| 78  | BI    | 266    |                  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 79  | BJ    | 349    |                  |
| 80  | BH    | 390    |                  |
| 81  | BN    | 69     |                  |
| 82  | BM    | 79     |                  |
| 83  | BO    | 30     |                  |
| 84  | BL    | 64     |                  |
| 85  | 2     | 1743   |                  |
| 86  | Az    | 109    |                  |
| 87  | Ah    | 171    |                  |
| 88  | BK    | 316    |                  |
| 89  | Bk    | 125    |                  |

## 2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 189336 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal protein L2, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 1   | Aa    | 96       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 753   | 465 | 152 | 133 | 3 |         |       |

- Molecule 2 is a protein called Expressed protein.

| Mol | Chain | Residues | Atoms |     |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 2   | Ab    | 155      | Total | C   | N   | O   | S  | 0       | 0     |
|     |       |          | 1144  | 709 | 224 | 200 | 11 |         |       |

- Molecule 3 is a protein called 50S ribosomal protein L3-2, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3   | Ac    | 218      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1674  | 1058 | 318 | 288 | 10 |         |       |

- Molecule 4 is a protein called Ribosomal protein L35.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 4   | AD    | 60       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 506   | 327 | 102 | 76 | 1 |         |       |

- Molecule 5 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5   | Ad    | 209      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1649  | 1043 | 311 | 288 | 7 |         |       |

- Molecule 6 is a protein called 60S ribosomal protein L5, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 6   | Ae    | 144      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1171  | 760 | 191 | 212 | 8 |         |       |

- Molecule 7 is a protein called Putative ribosomal protein L6.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 7   | Af    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 797   | 517 | 141 | 134 | 5 |         |       |

- Molecule 8 is a protein called Ribosomal protein L9/RNase H1.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 8   | Ag    | 51       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 406   | 265 | 70 | 70 | 1 |         |       |

- Molecule 9 is a protein called At4g35490.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 9   | Ai    | 138      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1056  | 677 | 182 | 190 | 7 |         |       |

- Molecule 10 is a protein called At1g01640.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10  | Aj    | 155      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1267  | 800 | 244 | 217 | 6 |         |       |

- Molecule 11 is a protein called 50S ribosomal protein HLP, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 11  | Ak    | 127      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 962   | 605 | 183 | 169 | 5 |         |       |

- Molecule 12 is a protein called Ribosomal protein L18e/L15 superfamily protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12  | Al    | 180      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1407  | 897 | 274 | 234 | 2 |         |       |

- Molecule 13 is a protein called 60S ribosomal protein L16, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13  | Am    | 142      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1111  | 702 | 219 | 182 | 8 |         |       |

- Molecule 14 is a protein called At5g09770.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 14  | An    | 141      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1139  | 708 | 228 | 198 | 5 |         |       |

- Molecule 15 is a protein called At5g27820.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15  | Ao    | 106      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 835   | 532 | 152 | 146 | 5 |         |       |

- Molecule 16 is a protein called At1g24240/F3I6\_17.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16  | Ap    | 114      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 935   | 600 | 178 | 155 | 2 |         |       |

- Molecule 17 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17  | Aq    | 106      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 888   | 557 | 178 | 148 | 5 |         |       |

- Molecule 18 is a protein called 50S ribosomal protein L21, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 18  | Ar    | 137      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1106  | 707 | 196 | 201 | 2 |         |       |

- Molecule 19 is a protein called AT1G52370 protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19  | As    | 121      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 937   | 587 | 184 | 163 | 3 |         |       |

- Molecule 20 is a protein called At4g39880.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20  | At    | 105      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 840   | 545 | 148 | 145 | 2 |         |       |

- Molecule 21 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21  | Au    | 142      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1112  | 702 | 210 | 196 | 4 |         |       |

- Molecule 22 is a protein called Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22  | Av    | 198      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1523  | 968 | 270 | 281 | 4 |         |       |

- Molecule 23 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23  | Aw    | 76       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 606   | 387 | 117 | 102 |   |         |       |

- Molecule 24 is a protein called AT4g31460/F3L17\_30.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24  | Ax    | 99       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 809   | 511 | 151 | 143 | 4 |         |       |

- Molecule 25 is a protein called At1g07830/F24B9\_7.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25  | Ay    | 111      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 943   | 592 | 175 | 168 | 8 |         |       |

- Molecule 26 is a protein called Ribosomal protein L31.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 26  | AA    | 37       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 299   | 187 | 57 | 54 | 1 |         |       |

- Molecule 27 is a protein called At1g26740/T24P13\_11.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 27  | AB    | 41       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 319   | 203 | 67 | 45 | 4 |         |       |

- Molecule 28 is a protein called At3g06320.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 28  | AC    | 51       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 432   | 283 | 77 | 70 | 2 |         |       |

- Molecule 29 is a protein called Ribosomal protein.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 29  | AE    | 36       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 297   | 183 | 63 | 47 | 4 |         |       |

- Molecule 30 is a protein called At4g05400.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30  | AF    | 84       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 663   | 419 | 115 | 127 | 2 |         |       |

- Molecule 31 is a protein called At5g40080.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 31  | AG    | 61       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 485   | 316 | 84 | 83 | 2 |         |       |

- Molecule 32 is a protein called Mitochondrial ribosomal protein L51/S25/CI-B8 family protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32  | AH    | 110      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 879   | 553 | 168 | 154 | 4 |         |       |

- Molecule 33 is a protein called At1g14620/T5E21\_15.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 33  | AI    | 207      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1714  | 1118 | 282 | 306 | 8 |         |       |

- Molecule 34 is a protein called 39S ribosomal protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34  | AJ    | 81       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 632   | 392 | 115 | 121 | 4 |         |       |

- Molecule 35 is a protein called At4g22000.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35  | AK    | 87       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 732   | 456 | 143 | 125 | 8 |         |       |

- Molecule 36 is a protein called Uncharacterized protein At1g27435/F17L21.30.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 36  | AL    | 52       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 400   | 246 | 82 | 71 | 1 |         |       |

- Molecule 37 is a protein called At1g73940/F2P9\_19.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 37  | AM    | 82       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 651   | 425 | 114 | 108 | 4 |         |       |

- Molecule 38 is a protein called At3g51010.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 38  | AN    | 80       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 664   | 406 | 141 | 115 | 2 |         |       |

- Molecule 39 is a protein called Pentatricopeptide repeat-containing protein At1g60770.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 39  | AO    | 452      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 3595  | 2276 | 615 | 682 | 22 |         |       |

- Molecule 40 is a protein called rPPR\*.

| Mol | Chain | Residues | Atoms |      |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---------|-------|
| 40  | AP    | 669      | Total | C    | N   | O   | 0       | 0     |
|     |       |          | 3345  | 2007 | 669 | 669 |         |       |

- Molecule 41 is a protein called Pentatricopeptide repeat-containing protein PNM1, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 41  | AQ    | 366      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2900  | 1835 | 501 | 537 | 27 |         |       |

- Molecule 42 is a protein called UNK-6.

| Mol | Chain | Residues | Atoms |    |    |    | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---------|-------|
| 42  | AR    | 29       | Total | C  | N  | O  | 0       | 0     |
|     |       |          | 145   | 87 | 29 | 29 |         |       |

- Molecule 43 is a RNA chain called RNA (2842-MER).

| Mol | Chain | Residues | Atoms |       |       |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 43  | 1     | 2842     | Total | C     | N     | O     | P    | 6       | 0     |
|     |       |          | 60842 | 27171 | 11068 | 19760 | 2843 |         |       |

- Molecule 44 is a RNA chain called RNA (118-MER).

| Mol | Chain | Residues | Atoms |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 44  | 3     | 118      | Total | C    | N   | O   | P   | 0       | 0     |
|     |       |          | 2513  | 1124 | 453 | 819 | 117 |         |       |

- Molecule 45 is a protein called Ribosomal protein S3, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 45  | Bb    | 281      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 2293  | 1489 | 413 | 383 | 8 |         |       |

- Molecule 46 is a protein called Ribosomal protein S7, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 46  | Bf    | 136      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1106  | 699 | 216 | 187 | 4 |         |       |

- Molecule 47 is a protein called 30S ribosomal protein S9, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 47  | Bh    | 123      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 975   | 616 | 187 | 168 | 4 |         |       |

- Molecule 48 is a protein called 40S ribosomal protein S10, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 48  | Bi    | 101      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 857   | 556 | 161 | 135 | 5 |         |       |

- Molecule 49 is a protein called Small ribosomal subunit protein S13, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 49  | Bl    | 91       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 729   | 442 | 153 | 132 | 2 |         |       |

- Molecule 50 is a protein called At2g34520.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 50  | Bm    | 96       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 794   | 495 | 165 | 130 | 4 |         |       |

- Molecule 51 is a protein called 40S ribosomal protein S19, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 51  | Br    | 83       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 685   | 439 | 130 | 112 | 4 |         |       |

- Molecule 52 is a protein called Mitochondrial 28S ribosomal protein S29-like protein.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 52  | Bw    | 337      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2722  | 1752 | 469 | 488 | 13 |         |       |

- Molecule 53 is a protein called 37S ribosomal protein S27.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 53  | Bx    | 79       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 641   | 402 | 125 | 112 | 2 |         |       |

- Molecule 54 is a protein called AT3G18240 protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 54  | Bz    | 123      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1010  | 634 | 198 | 175 | 3 |         |       |

- Molecule 55 is a protein called CX9C domain-containing protein.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 55  | BA    | 38       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 293   | 181 | 50 | 54 | 8 |         |       |

- Molecule 56 is a protein called 30S ribosomal protein S31, mitochondrial.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 56  | Bt    | 29       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 239   | 149 | 50 | 39 | 1 |         |       |

- Molecule 57 is a protein called Pentatricopeptide repeat-containing protein At3g02650, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|--|---------|-------|
| 57  | BG    | 364      | Total | C    | N   | O   |  | 0       | 0     |
|     |       |          | 1795  | 1067 | 364 | 364 |  |         |       |

- Molecule 58 is a protein called UNK-5.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 58  | BP    | 91       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 455   | 273 | 91 | 91 |  |         |       |

- Molecule 59 is a protein called mS31/mS46.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 59  | BF    | 123      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 615   | 369 | 123 | 123 |  |         |       |

- Molecule 60 is a protein called Ribosomal protein S2, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 60  | Ba    | 195      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1563  | 1003 | 276 | 273 | 11 |         |       |

- Molecule 61 is a protein called Ribosomal protein S4, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 61  | Bc    | 327      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2772  | 1781 | 526 | 454 | 11 |         |       |

- Molecule 62 is a protein called At1g64880.

| Mol | Chain | Residues | Atoms |      |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 62  | Bd    | 216      | Total | C    | N   | O   | S | 0       | 0     |
|     |       |          | 1730  | 1097 | 310 | 317 | 6 |         |       |

- Molecule 63 is a protein called Translation elongation factor EF1B/ribosomal protein S6 family protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63  | Be    | 99       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 819   | 529 | 147 | 137 | 6 |         |       |

- Molecule 64 is a protein called 40S ribosomal protein S15a-5.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64  | Bg    | 128      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1042  | 657 | 194 | 188 | 3 |         |       |

- Molecule 65 is a protein called Probable ribosomal protein S11, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65  | Bj    | 123      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 955   | 590 | 188 | 172 | 5 |         |       |

- Molecule 66 is a protein called At1g15810/F7H2\_23.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66  | Bn    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 814   | 509 | 150 | 149 | 6 |         |       |

- Molecule 67 is a protein called 30S ribosomal protein S16-2, chloroplastic/mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67  | Bo    | 99       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 780   | 496 | 152 | 127 | 5 |         |       |

- Molecule 68 is a protein called Nucleic acid-binding, OB-fold-like protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68  | Bp    | 78       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 636   | 405 | 120 | 108 | 3 |         |       |

- Molecule 69 is a protein called F10K1.8 protein.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 69  | Bq    | 62       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 492   | 313 | 91 | 87 | 1 |         |       |

- Molecule 70 is a protein called Ribosomal protein S21 family protein.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 70  | Bs    | 66       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 539   | 337 | 106 | 94 | 2 |         |       |

- Molecule 71 is a protein called Uncharacterized protein.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71  | Bu    | 100      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 800   | 508 | 147 | 140 | 5 |         |       |

- Molecule 72 is a protein called AT5g49210/K21P3\_8.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72  | Bv    | 149      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1278  | 800 | 237 | 237 | 4 |         |       |

- Molecule 73 is a protein called 28S ribosomal S34 protein.

| Mol | Chain | Residues | Atoms |     |     |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 73  | By    | 76       | Total | C   | N   | O  | S | 0       | 0     |
|     |       |          | 619   | 404 | 115 | 98 | 2 |         |       |

- Molecule 74 is a protein called mS38.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 74  | BB    | 23       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 203   | 129 | 46 | 27 | 1 |         |       |

- Molecule 75 is a protein called At5g26800.

| Mol | Chain | Residues | Atoms |     |    |    |   | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 75  | BC    | 68       | Total | C   | N  | O  | S | 0       | 0     |
|     |       |          | 544   | 356 | 99 | 88 | 1 |         |       |

- Molecule 76 is a protein called Gb|AAC32909.1.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 76  | BD    | 210      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 1768  | 1113 | 317 | 328 | 10 |         |       |

- Molecule 77 is a protein called 3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial.

| Mol | Chain | Residues | Atoms |      |     |     |    | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 77  | BE    | 348      | Total | C    | N   | O   | S  | 0       | 0     |
|     |       |          | 2697  | 1716 | 446 | 517 | 18 |         |       |

- Molecule 78 is a protein called rPPR\*.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 78  | BI    | 266      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1330  | 798 | 266 | 266 |  |         |       |

- Molecule 79 is a protein called rPPR\*.

| Mol | Chain | Residues | Atoms |      |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|--|---------|-------|
| 79  | BJ    | 349      | Total | C    | N   | O   |  | 0       | 0     |
|     |       |          | 1745  | 1047 | 349 | 349 |  |         |       |

- Molecule 80 is a protein called Adenylyl cyclase.

| Mol | Chain | Residues | Atoms |     |     |     |  | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|-------|
| 80  | BH    | 206      | Total | C   | N   | O   |  | 0       | 0     |
|     |       |          | 1023  | 611 | 206 | 206 |  |         |       |

- Molecule 81 is a protein called UNK-3.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 81  | BN    | 69       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 345   | 207 | 69 | 69 |  |         |       |

- Molecule 82 is a protein called UNK-2.

| Mol | Chain | Residues | Atoms |     |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|-------|
| 82  | BM    | 79       | Total | C   | N  | O  |  | 0       | 0     |
|     |       |          | 395   | 237 | 79 | 79 |  |         |       |

- Molecule 83 is a protein called UNK-4.

| Mol | Chain | Residues | Atoms |    |    |    |  | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|--|---------|-------|
| 83  | BO    | 30       | Total | C  | N  | O  |  | 0       | 0     |
|     |       |          | 150   | 90 | 30 | 30 |  |         |       |

- Molecule 84 is a protein called UNK-1.

| Mol | Chain | Residues | Atoms |     |    |    | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|-------|
| 84  | BL    | 64       | Total | C   | N  | O  | 0       | 0     |
|     |       |          | 320   | 192 | 64 | 64 |         |       |

- Molecule 85 is a RNA chain called RNA (1743-MER).

| Mol | Chain | Residues | Atoms |       |      |       |      | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 85  | 2     | 1743     | Total | C     | N    | O     | P    | 0       | 0     |
|     |       |          | 37379 | 16678 | 6858 | 12100 | 1743 |         |       |

- Molecule 86 is a protein called At5g55140.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 86  | Az    | 82       | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 660   | 406 | 135 | 114 | 5 |         |       |

- Molecule 87 is a protein called 50S ribosomal protein L10.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 87  | Ah    | 137      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 1098  | 706 | 187 | 200 | 5 |         |       |

- Molecule 88 is a protein called rPPR\*.

| Mol | Chain | Residues | Atoms |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|-------|
| 88  | BK    | 316      | Total | C   | N   | O   | 0       | 0     |
|     |       |          | 1580  | 948 | 316 | 316 |         |       |

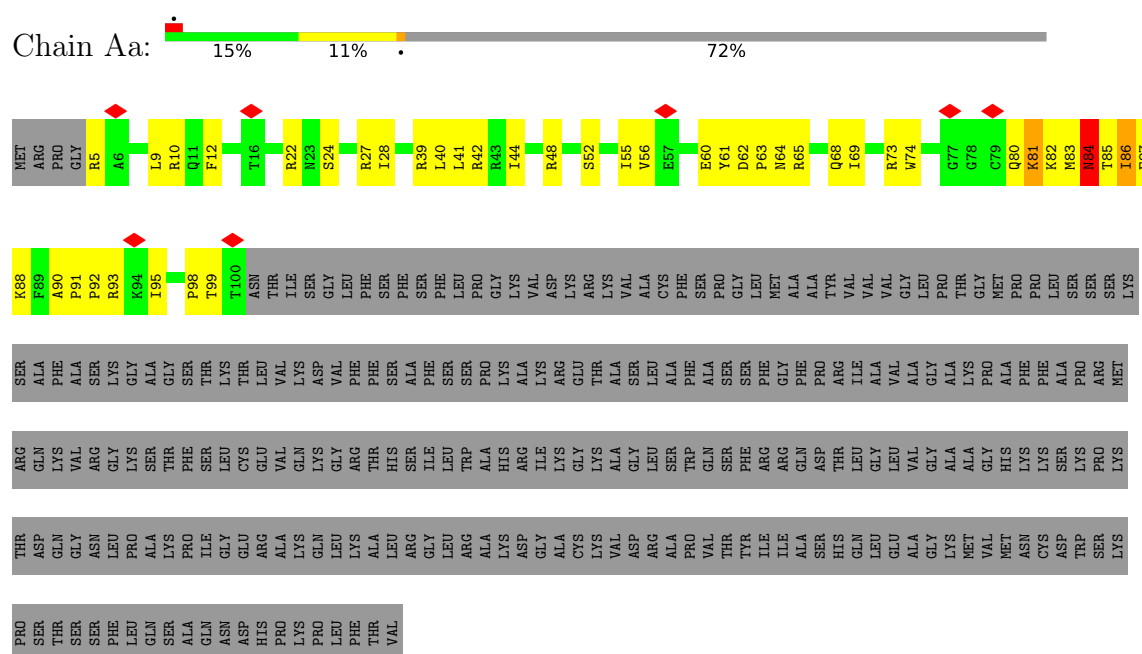
- Molecule 89 is a protein called Ribosomal protein S12, mitochondrial.

| Mol | Chain | Residues | Atoms |     |     |     |   | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 89  | Bk    | 121      | Total | C   | N   | O   | S | 0       | 0     |
|     |       |          | 968   | 598 | 204 | 162 | 4 |         |       |

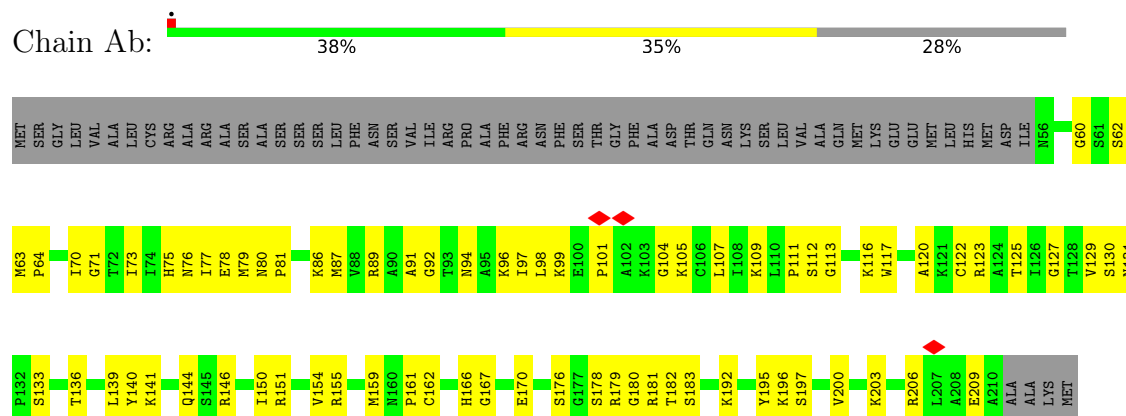
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 60S ribosomal protein L2, mitochondrial



- Molecule 2: Expressed protein



- Molecule 3: 50S ribosomal protein L3-2, mitochondrial

- Molecule 4: Ribosomal protein L35

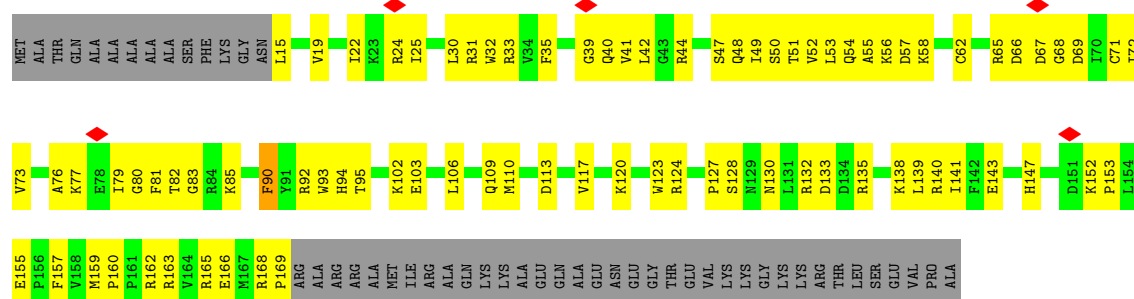
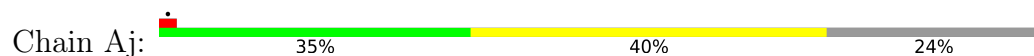
- Molecule 5: 50S ribosomal protein L4

- Molecule 6: 60S ribosomal protein L5, mitochondrial

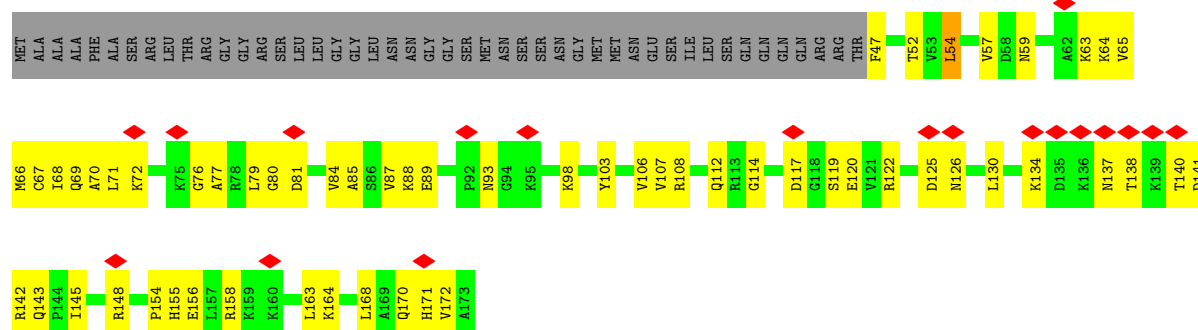




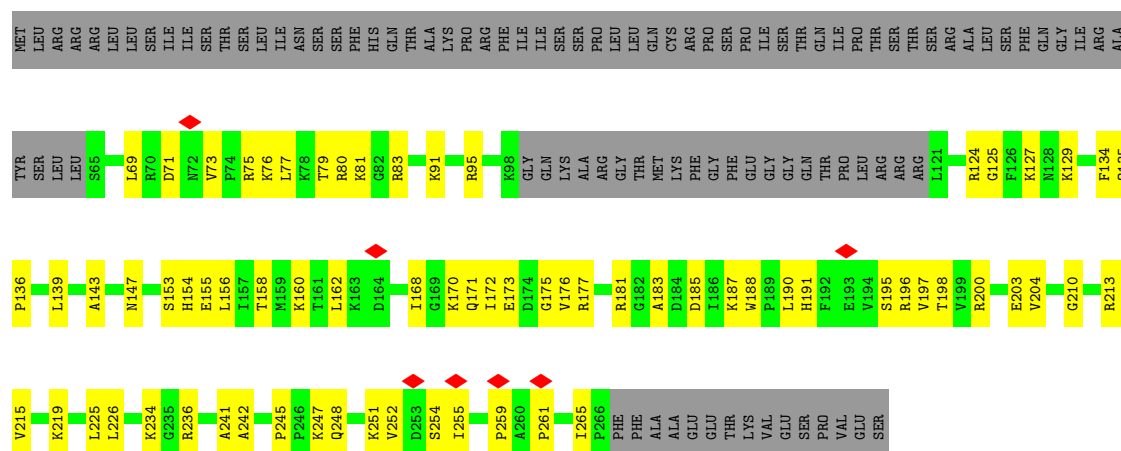
• Molecule 10: At1g01640



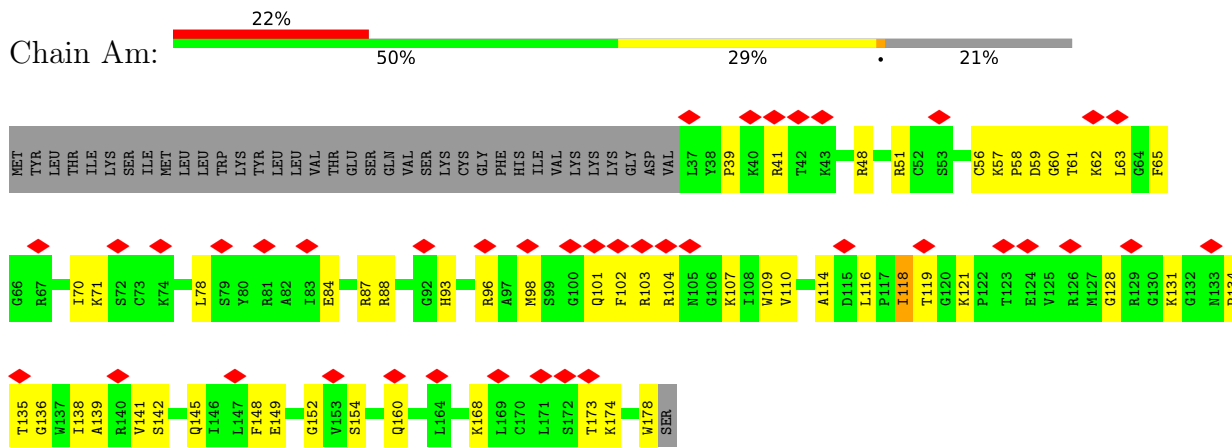
• Molecule 11: 50S ribosomal protein HLP, mitochondrial



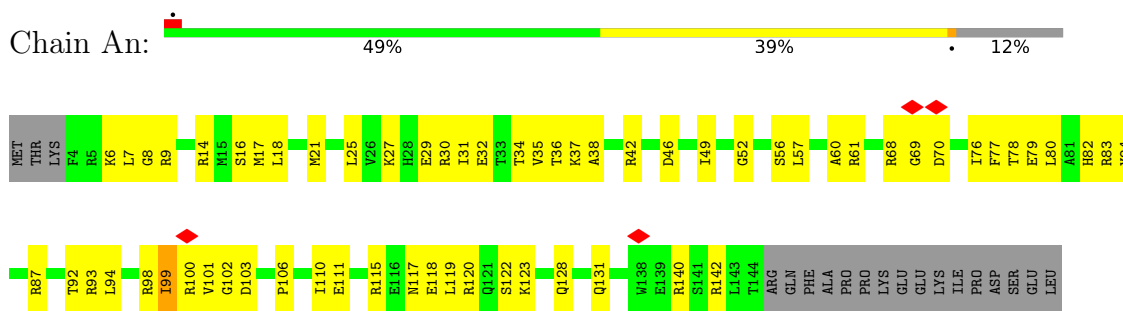
• Molecule 12: Ribosomal protein L18e/L15 superfamily protein



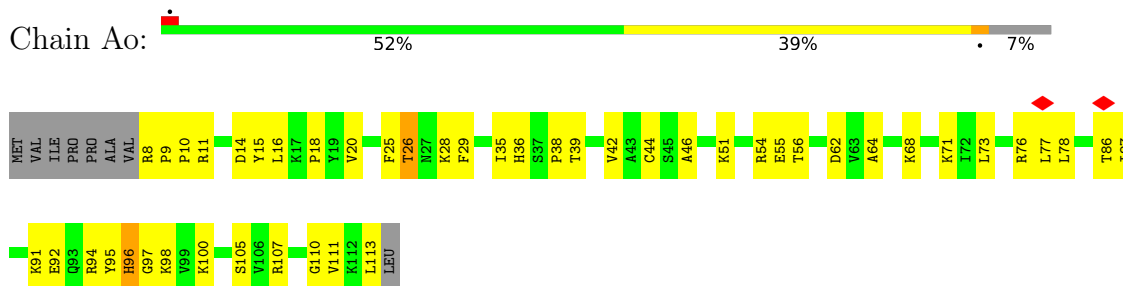
- Chain Am:



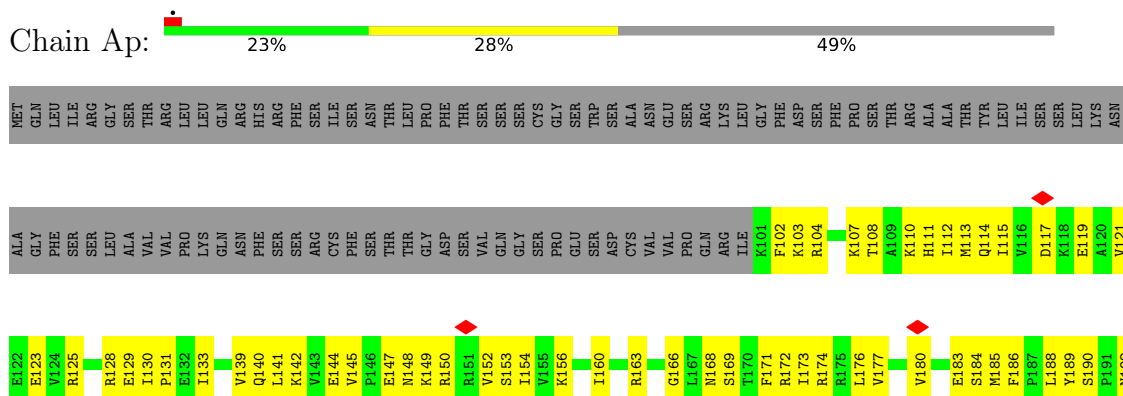
- Chain An:



- Chain Ao:

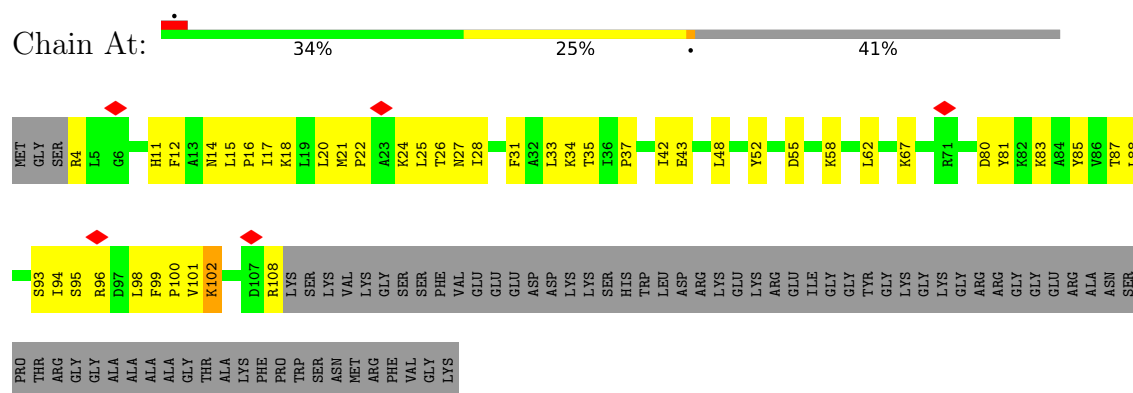


- Chain Ap:

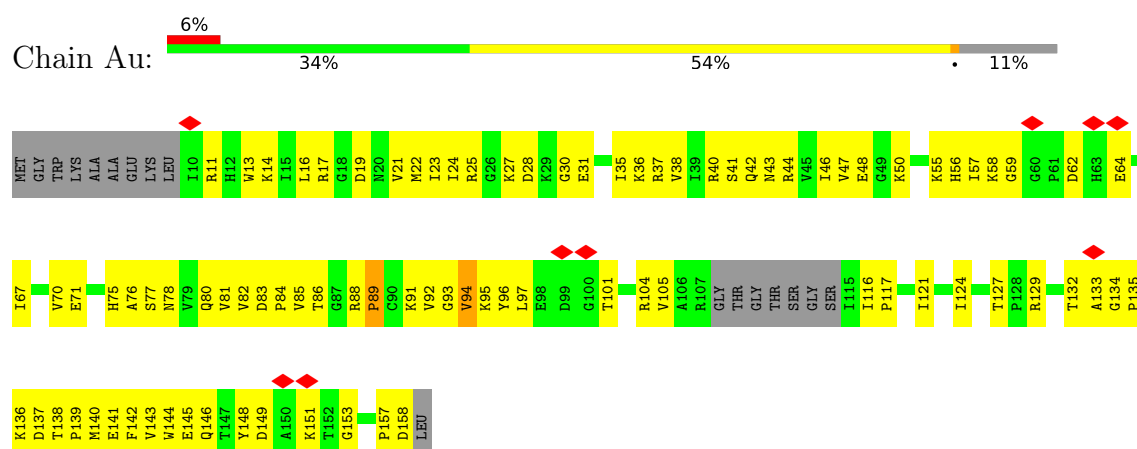




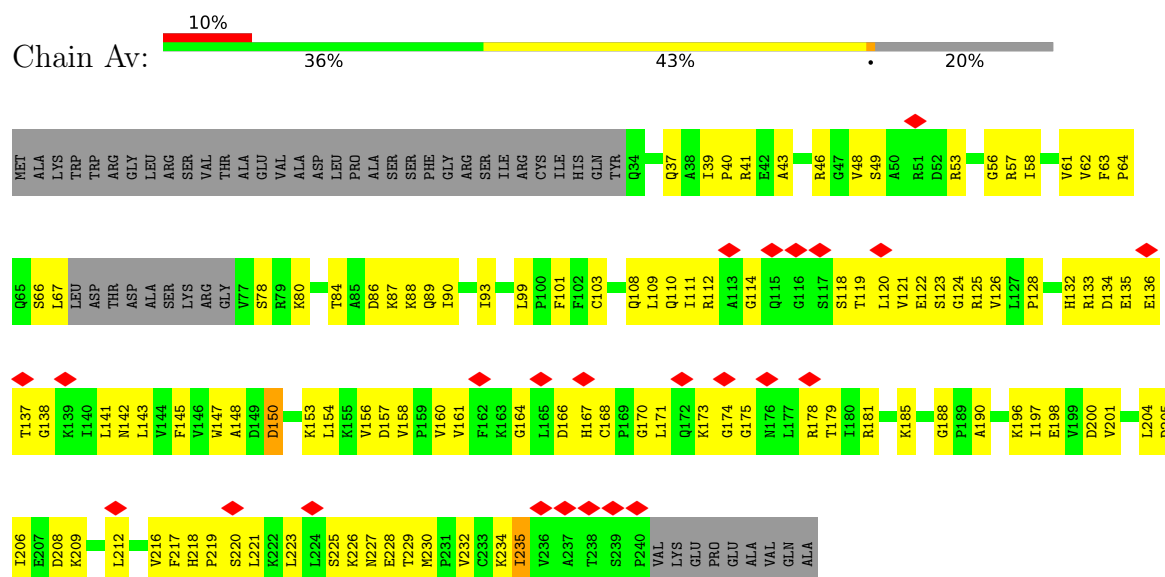
- Molecule 20: At4g39880



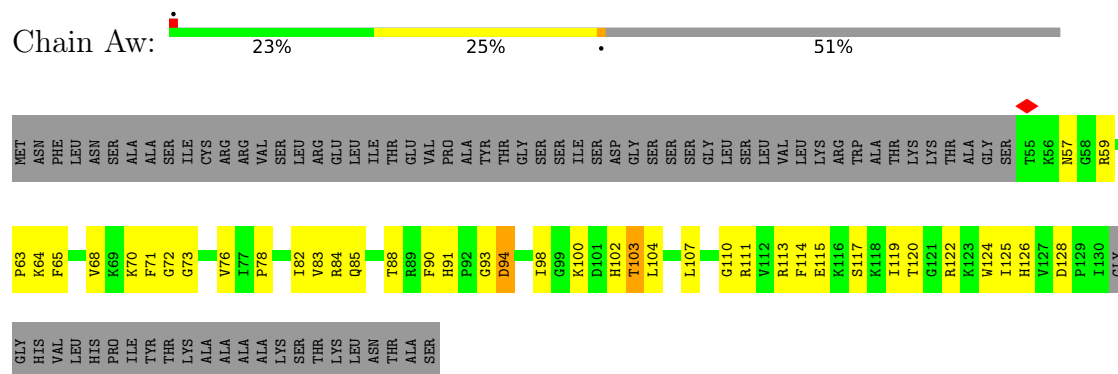
- Molecule 21: 50S ribosomal protein L24



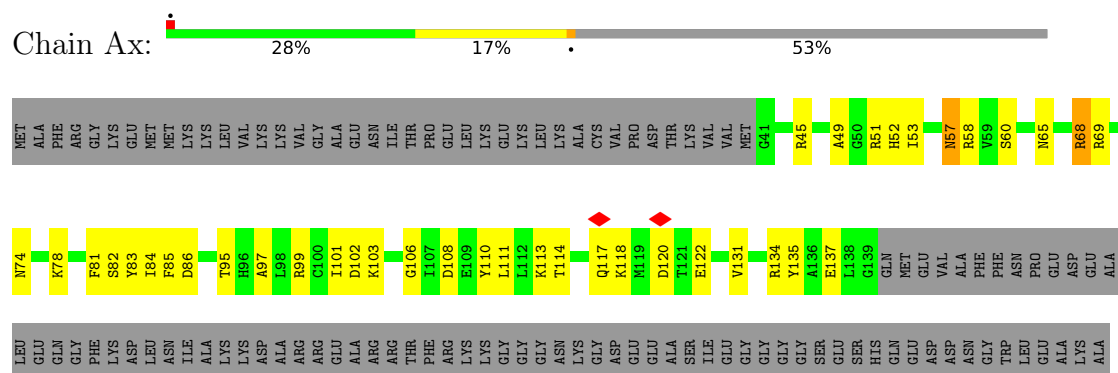
- Molecule 22: Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding domain-containing protein



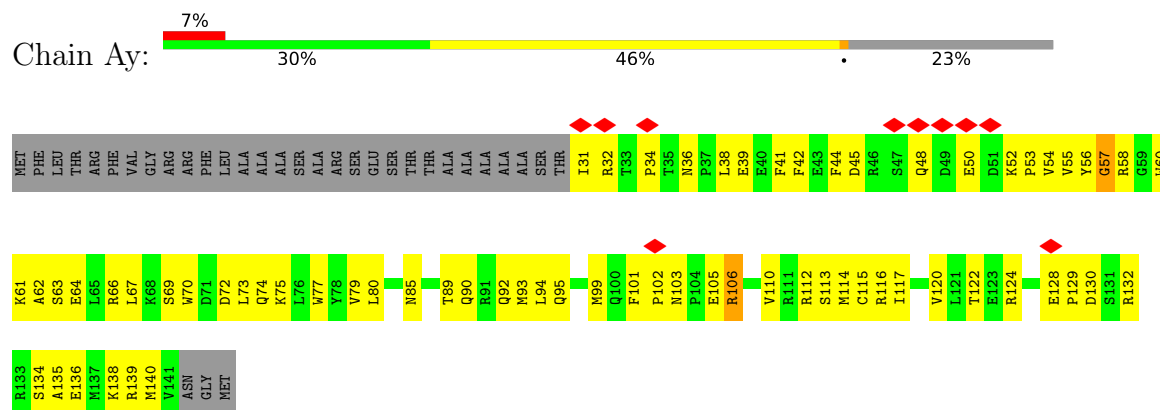
- Molecule 23: 50S ribosomal protein L27



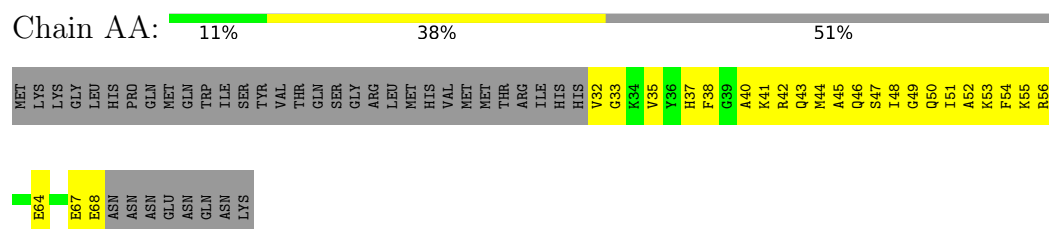
• Molecule 24: AT4g31460/F3L17\_30



• Molecule 25: At1g07830/F24B9\_7

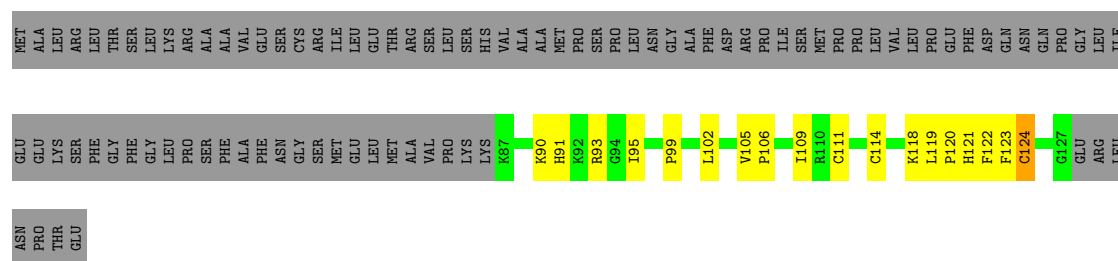


• Molecule 26: Ribosomal protein L31



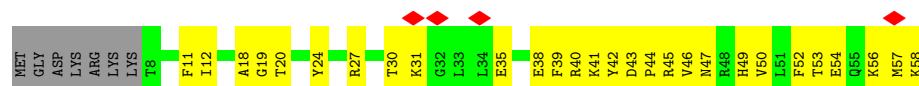
• Molecule 27: At1g26740/T24P13\_11

Chain AB: 



• Molecule 28: At3g06320

Chain AC: 



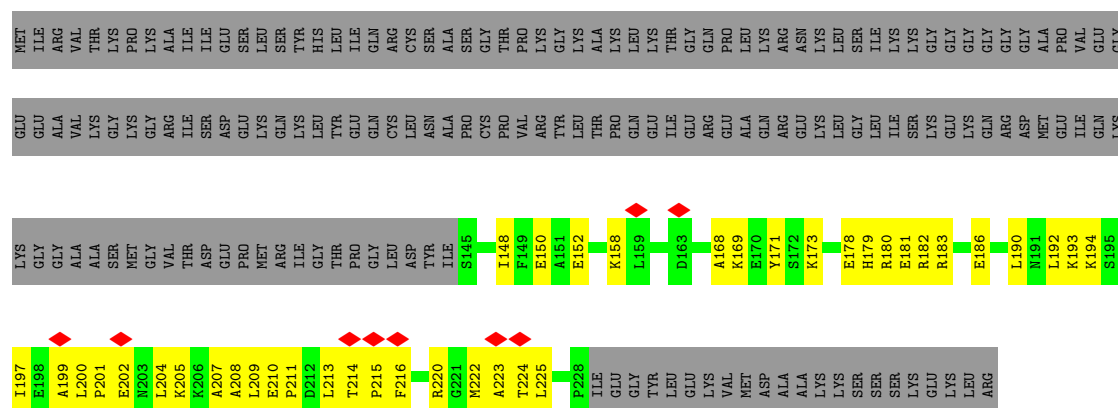
• Molecule 29: Ribosomal protein

Chain AE: 

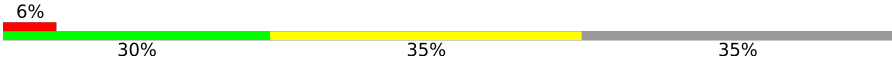


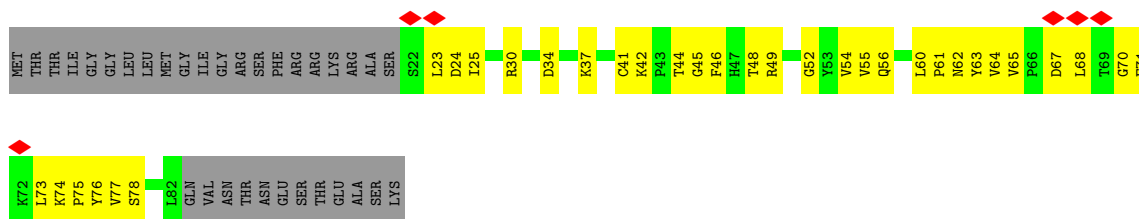
• Molecule 30: At4g05400

Chain AF: 

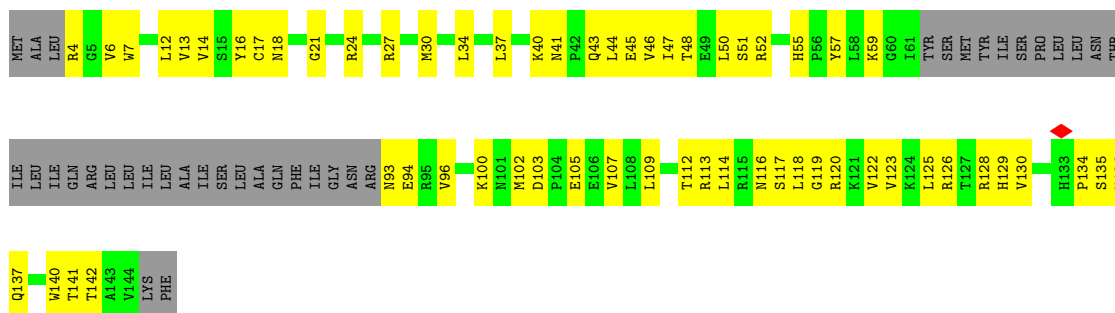


• Molecule 31: At5g40080

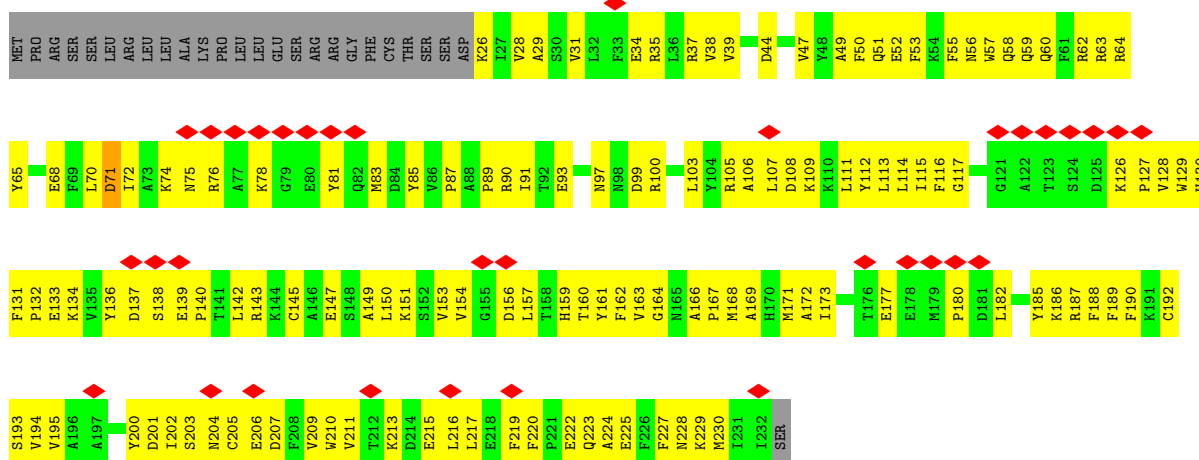
Chain AG: 



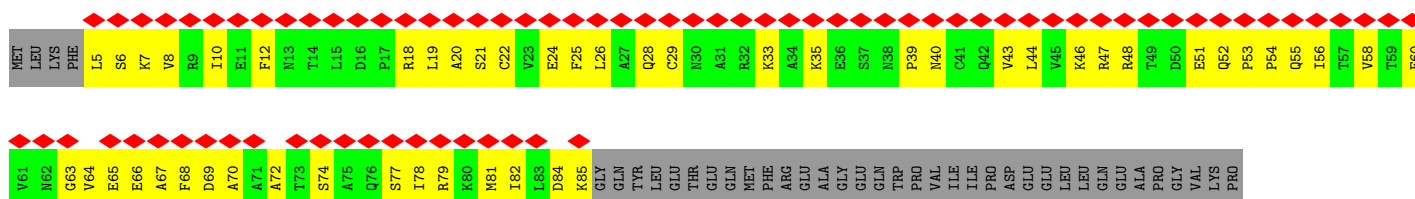
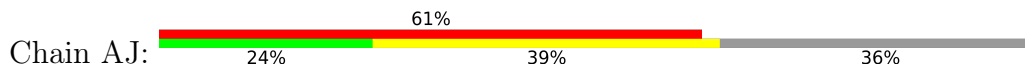
- Molecule 32: Mitochondrial ribosomal protein L51/S25/CI-B8 family protein



- Molecule 33: At1g14620/T5E21\_15



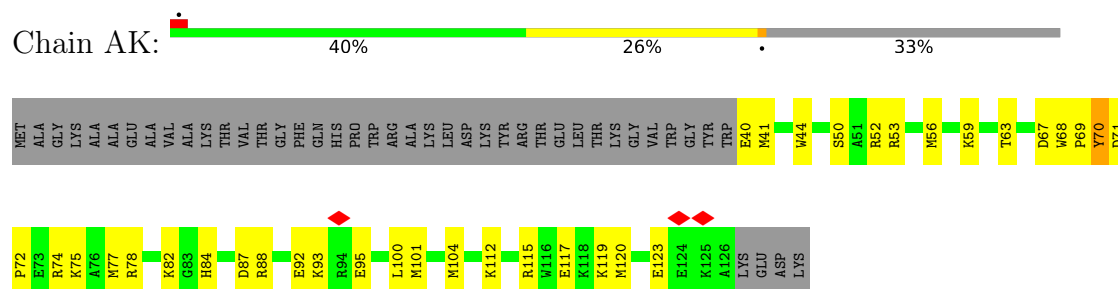
- Molecule 34: 39S ribosomal protein



ARG  
LYS  
ALA  
GLU  
ASP  
LYS  
LYS

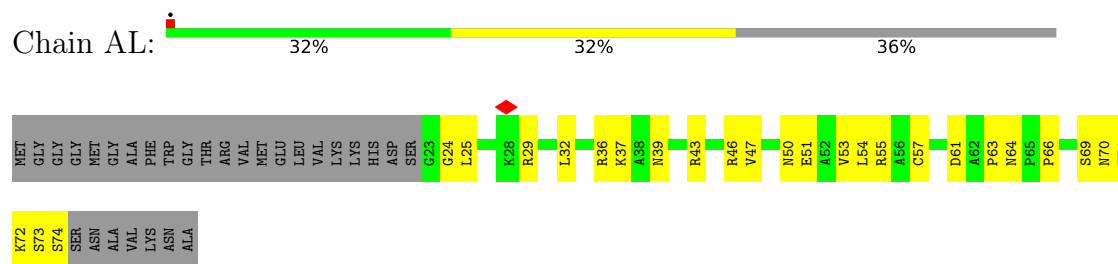
• Molecule 35: At4g22000

Chain AK:



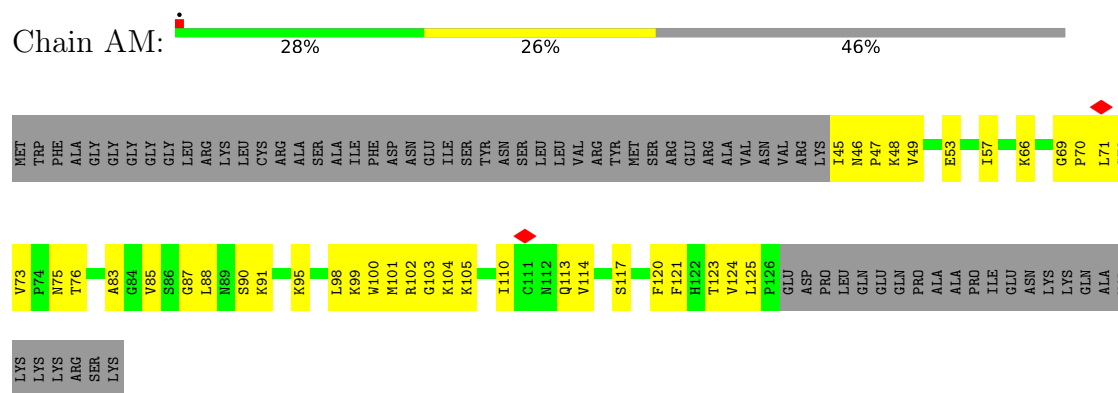
• Molecule 36: Uncharacterized protein At1g27435/F17L21.30

Chain AL:



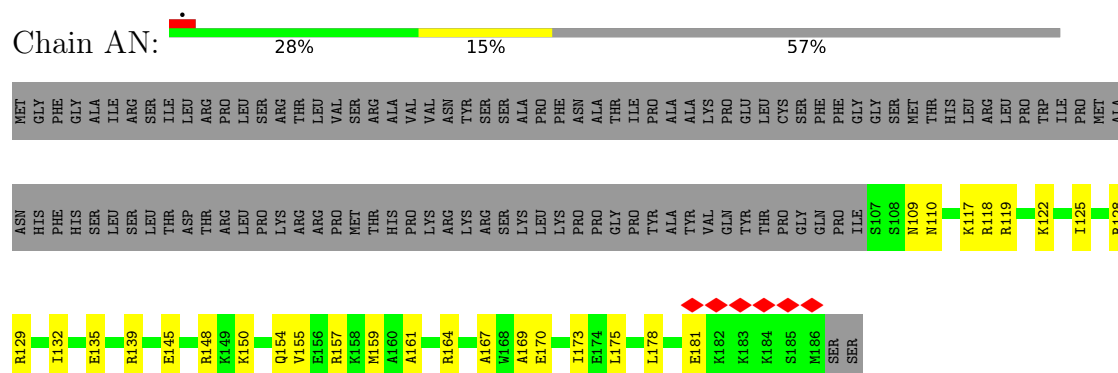
• Molecule 37: At1g73940/F2P9\_19

Chain AM:

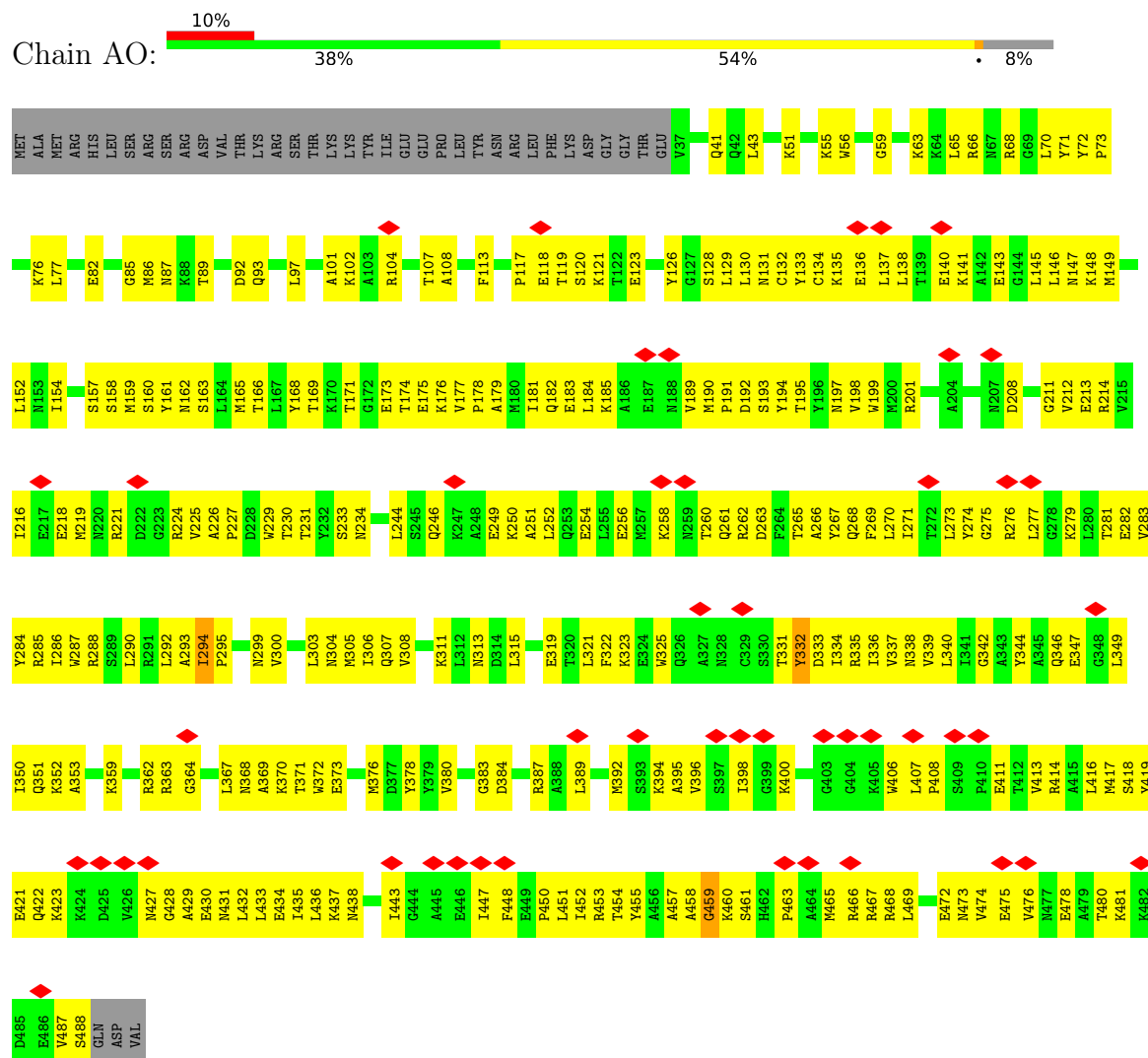


• Molecule 38: At3g51010

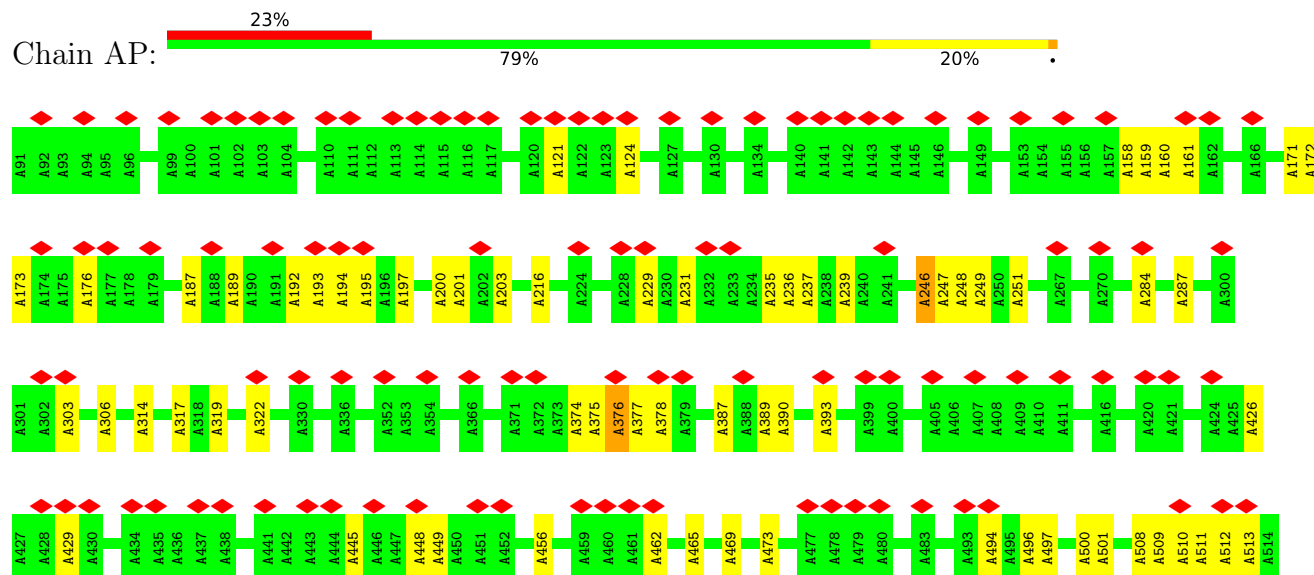
Chain AN:



- Molecule 39: Pentatricopeptide repeat-containing protein At1g60770



- Molecule 40: rPPR\*



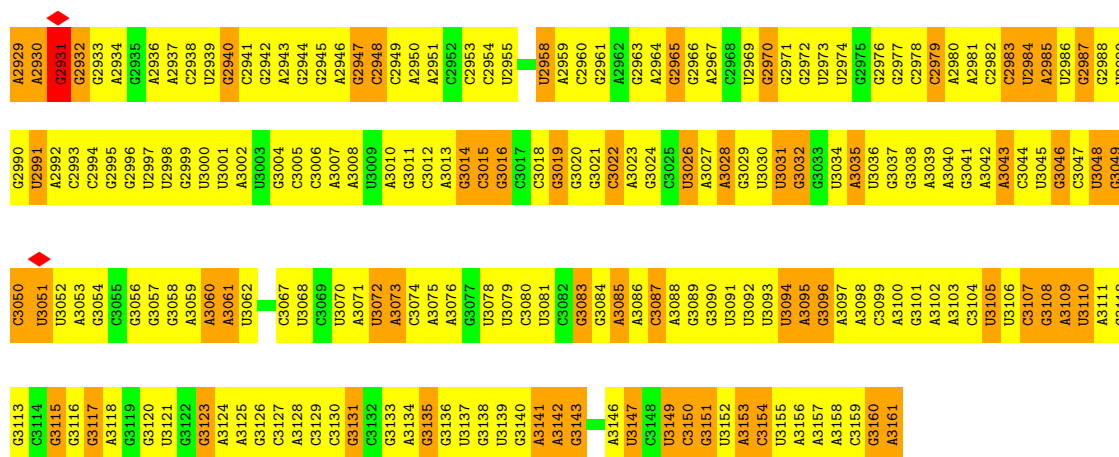


Chain 1: 

|                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                               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| G16<br>A17<br>A18<br>A19<br>G20<br>G21<br>G22<br>A22<br>U23<br>U24<br>G25<br>G26<br>A27<br>U28<br>G29<br>G30<br>A31<br>U32<br>G33<br>G34<br>G35<br>G36<br>G37<br>G38<br>G39<br>C40<br>A41<br>U42<br>G43<br>G44<br>A45<br>G46<br>G47<br>G48<br>G49<br>G50<br>G51<br>A52<br>G53<br>G54<br>G55<br>G56<br>G57<br>G58<br>U59<br>U60<br>G61<br>G62<br>G63<br>G64<br>G65<br>G66<br>G67<br>G68<br>G69<br>A70<br>A71<br>A72<br>G73<br>G74<br>G75 | G76<br>A77<br>U78<br>G79<br>G80<br>G81<br>G82<br>G83<br>G84<br>G85<br>G86<br>G87<br>G88<br>G89<br>G90<br>U91<br>C92<br>G93<br>G94<br>G95<br>G96<br>G97<br>G98<br>G99<br>C100<br>A101<br>U102<br>G103<br>G104<br>A105<br>U106<br>C109<br>G110<br>G111<br>A112<br>U113<br>G114<br>G115<br>G116<br>G117<br>G118<br>G119<br>A120<br>C121<br>G122<br>G123<br>U124<br>A125<br>U126<br>C127<br>G128<br>A129<br>G130<br>G131<br>C132<br>U133<br>G134<br>C135<br>G136 | U137<br>G138<br>C139<br>C140<br>U141<br>A142<br>G143<br>U144<br>C145<br>A146<br>G147<br>G148<br>G149<br>G150<br>U151<br>C152<br>U153<br>U154<br>G155<br>G156<br>G157<br>A158<br>C159<br>U160<br>G161<br>G162<br>A163<br>A164<br>A165<br>A166<br>A167<br>C168<br>U169<br>U170<br>A171<br>G172<br>C173<br>G174<br>A175<br>A176<br>G177<br>U178<br>G179<br>A180<br>A181<br>A182<br>C183<br>U184<br>U185<br>C186<br>A187<br>G188<br>A189<br>G190<br>U191<br>A192<br>G193<br>C194<br>A198 | G199<br>G200<br>A201<br>A202<br>G203<br>G204<br>G205<br>A206<br>A207<br>A208<br>G209<br>C210<br>C213<br>C214<br>G215<br>A216<br>G217<br>A218<br>C219<br>G220<br>C221<br>C222<br>G223<br>U224<br>U225<br>A226<br>G227<br>G228<br>G229<br>G230<br>C231<br>G232<br>C233<br>G234<br>G235<br>A236<br>G237<br>C238<br>G239<br>A240<br>G241<br>A242<br>G243<br>C244<br>G245<br>U249<br>G250<br>G251<br>G252<br>G253<br>A254<br>U255<br>U256<br>U257<br>U258<br>A259<br>G260<br>G261 | A262<br>A263<br>A264<br>A265<br>A266<br>G267<br>A268<br>A269<br>A270<br>G271<br>A272<br>C273<br>G274<br>A275<br>A276<br>G277<br>C278<br>A279<br>U298<br>C300<br>U301<br>U302<br>U303<br>U304<br>U305<br>G306<br>G307<br>C308<br>G309<br>A310<br>G311<br>G312<br>U313<br>U314<br>U315<br>A420<br>C421<br>U422<br>G423<br>U424<br>A425<br>A426<br>U427<br>U428<br>G429<br>U430<br>A431<br>A432<br>A433<br>A434<br>A435<br>C436<br>G437<br>G440<br>G441<br>A442<br>A443 | G444<br>G445<br>G446<br>C447<br>A448<br>G449<br>G450<br>C451<br>C452<br>A453<br>A454<br>A455<br>G456<br>A457<br>A458<br>G459<br>G460<br>U461<br>G462<br>A463<br>U464<br>A465<br>G466<br>G467<br>C468<br>C469<br>C470<br>G471<br>U472<br>A473<br>A474<br>A475<br>U476<br>U477<br>C478<br>G479<br>U480<br>U481<br>C482<br>C483<br>U484<br>A485<br>U486<br>G487<br>G488<br>U489<br>U490<br>C491<br>G492<br>A493<br>U494<br>C495<br>C496<br>U497<br>U498<br>C499<br>C500<br>C501<br>A502<br>G503<br>U504<br>A505<br>A506 | A507<br>A508<br>C509<br>G510<br>C511<br>G512<br>G513<br>C514<br>G515<br>U516<br>U517<br>U518<br>U519<br>C520<br>G521<br>A522<br>A523<br>U524<br>U525<br>C526<br>U527<br>G528<br>A529<br>U530<br>C531<br>G532<br>C533<br>U534<br>U535<br>U536<br>U537<br>A538<br>C539<br>G540<br>C541<br>G542<br>A543<br>G544<br>A545<br>A546<br>A547<br>G548<br>G549<br>G550<br>G551<br>G552<br>A553<br>C554<br>G555<br>A556<br>C557<br>C558<br>C559<br>U560<br>C561<br>U562<br>A563<br>A564<br>G565<br>C566 | C567<br>U568<br>A569<br>A570<br>G571<br>U572<br>A573<br>U574<br>U575<br>C576<br>C577<br>A580<br>A581<br>U582<br>G583<br>A584<br>C585<br>C586<br>G587<br>A590<br>C592<br>G593<br>U594<br>C595<br>A596<br>G597<br>A600<br>G604<br>U605<br>G606<br>A607<br>G608<br>G609<br>G610<br>A611<br>A612<br>G613<br>G614<br>G615<br>U616<br>G617<br>A618<br>A619<br>A620<br>A621<br>G622<br>A623<br>G624<br>A625<br>G626<br>C627<br>U628<br>A629 | U630<br>G631<br>A632<br>C633<br>A634<br>G635<br>G636<br>A637<br>G638<br>U639<br>U640<br>C641<br>A642<br>A643<br>U644<br>A645<br>G646<br>A647<br>G648<br>A649<br>A650<br>C651<br>A655<br>G656<br>C659<br>C660<br>G661<br>A662<br>U663<br>G664<br>C665<br>G666<br>A667<br>A670<br>U672<br>G673<br>A674<br>G675<br>G676<br>G677<br>A678<br>A679<br>A680<br>G681<br>G682<br>U685<br>A686<br>G687<br>U688<br>C689<br>A690<br>A691<br>G692<br>C693<br>G694<br>C695 | A696<br>C697<br>U698<br>C699<br>A700<br>G701<br>U702<br>C703<br>U704<br>A705<br>A706<br>C707<br>G708<br>G709<br>C710<br>G711<br>U712<br>U713<br>A714<br>C715<br>G716<br>U717<br>U718<br>U719<br>G720<br>C721<br>A722<br>U723<br>G724<br>A725<br>U726<br>G727<br>G728<br>G729<br>U730<br>A731<br>C732<br>G733<br>G734<br>G735<br>A736<br>G737<br>G738<br>A739<br>A740<br>A741<br>U742<br>G743<br>G744<br>G745<br>A746<br>G747<br>G748<br>A749<br>G750<br>G753<br>G754<br>U755<br>U756 | A757<br>A758<br>G759<br>C760<br>C761<br>A762<br>U763<br>U764<br>A765<br>G766<br>G767<br>U768<br>G769<br>U770<br>A771<br>G772<br>C773<br>G774<br>G775<br>G776<br>U777<br>U778<br>U779<br>C780<br>G781<br>A782<br>A783<br>U784<br>G785<br>G786<br>A787<br>U788<br>G789<br>U790<br>A791<br>A792<br>G793<br>U794<br>U795<br>C796<br>U797<br>A798<br>G799<br>U800<br>U801<br>C802<br>U803<br>U804<br>C805<br>C806<br>U807<br>A808<br>U809<br>U810<br>U811<br>G812<br>A813<br>C814<br>C815<br>C816 | G817<br>A818<br>C821<br>G822<br>C823<br>A824<br>U825<br>C826<br>A827<br>A828<br>U829<br>A832<br>G833<br>C834<br>G835<br>A836<br>U837<br>G838<br>A839<br>U840<br>C841<br>A842<br>G843<br>G844<br>U845<br>G846<br>A847<br>A848<br>A849<br>G850<br>A851<br>G852<br>A853<br>G854<br>C855<br>U856<br>C857<br>U858<br>A859<br>A860<br>C861<br>A862<br>G863<br>G864<br>U867<br>U868<br>G869<br>G870<br>A871<br>G872<br>G873<br>A874<br>C880<br>C881<br>C882 | G885<br>U886<br>A887<br>U888<br>G889<br>U890<br>G891<br>G892<br>C893<br>A894<br>C895<br>A896<br>G897<br>U898<br>G902<br>G903<br>G904<br>A905<br>U906<br>G907<br>U908<br>C909<br>G912<br>U913<br>G914<br>U917<br>A918<br>G919<br>G920<br>G921<br>G922<br>U923<br>A924<br>G925<br>A926<br>A927<br>G928<br>G929<br>C930<br>U931<br>C932<br>A933<br>C934<br>C935<br>G936<br>A937<br>G938<br>A939<br>U940<br>C941<br>G942<br>G943<br>U944<br>A945<br>U946<br>U947<br>A948 | G949<br>C950<br>U951<br>G952<br>G953<br>U954<br>G955<br>U956<br>U957<br>C958<br>C959<br>A959<br>G960<br>C961<br>G962<br>A963<br>G964<br>A965<br>U966<br>G967<br>U968<br>A969<br>U970<br>U971<br>U972<br>C973<br>A974<br>U975<br>G976<br>A977<br>G978<br>A979<br>G980<br>C981<br>G982<br>U983<br>A984<br>G985<br>A986<br>G987<br>U988<br>G989<br>U990<br>C991<br>G992<br>A993<br>U994<br>G995<br>G996<br>C997<br>C998<br>G999<br>U1000<br>A1001<br>G1002<br>G1003<br>U1004<br>A1005<br>U1006<br>A1007<br>G1008 |
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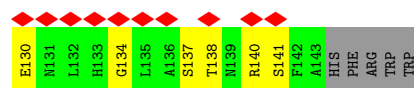
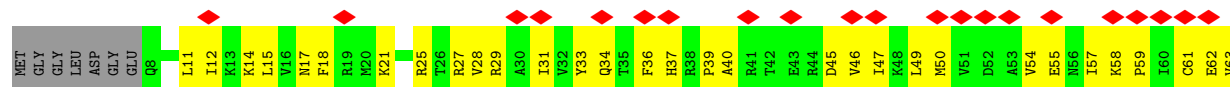
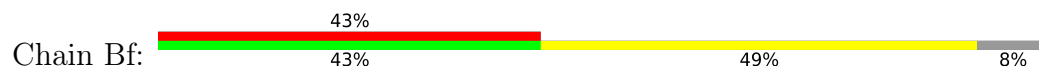
|       |       |       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| A1967 | U1905 | U1845 | C1631 | U1571 | C1508 | G1448 | G1386 | C1325 | C1264 | G1204 | U1143 | U1081 | C1009 |
| G1968 | U1906 | U1846 | C1632 | A1572 | U1509 | A1449 | A1387 | U1326 | C1265 | G1205 | A1144 | U1082 | A1010 |
| U1969 | G1907 | A1847 | U1633 | A1573 | A1510 | C1451 | C1388 | G1327 | U1266 | A1206 | C1145 | U1083 | C1011 |
| A1970 | G1908 | U1848 | C1634 | A1574 | A1511 | C1452 | C1389 | U1267 | U1268 | G1207 | C1146 | G1084 | U1012 |
| U1971 | G1909 | A1849 | U1635 | A1575 | G1512 | C1453 | U1390 | C1328 | C1268 | U1208 | C1147 | U1085 | C1013 |
| A1972 | A1910 | G1850 | U1636 | A1576 | G1513 | C1454 | G1391 | U1329 | G1269 | U1209 | U1148 | A1014 | A1014 |
| C1973 | G1911 | U1851 | C1637 | A1577 | A1514 | U1455 | G1392 | U1330 | G1270 | G1210 | A1149 | C1087 | A1015 |
| U1974 | G1912 | C1852 | C1638 | C1578 | A1515 | U1456 | A1393 | U1331 | C1271 | G1211 | A1150 | A1088 | A1016 |
| G1975 | G1913 | C1853 | C1639 | C1579 | C1519 | C1457 | G1394 | U1332 | C1272 | G1212 | G1151 | C1091 | U1017 |
| G1976 | G1914 | C1854 | C1640 | U1580 | C1520 | C1458 | A1395 | U1333 | A1275 | C1213 | C1154 | A1092 | G1018 |
| U1977 | G1915 | G1855 | U1641 | U1581 | C1521 | G1459 | U1396 | C1334 | A1276 | U1214 | C1155 | G1019 | G1019 |
| A1978 | A1916 | A1856 | C1642 | G1582 | G1522 | G1460 | A1397 | A1336 | A1277 | U1215 | C1156 | A1094 | C1020 |
| C1979 | U1917 | C1857 | A1643 | C1584 | A1523 | U1461 | U1398 | G1337 | A1278 | G1216 | U1157 | C1095 | U1021 |
| G1980 | C1918 | U1858 | U1644 | C1585 | A1524 | G1462 | C1399 | U1338 | U1279 | G1217 | A1158 | G1096 | A1022 |
| C1981 | C1919 | C1859 | U1645 | U1586 | G1525 | G1463 | A1401 | U1339 | U1280 | A1218 | A1159 | U1097 | G1023 |
| U1982 | G1920 | U1860 | C1646 | C1586 | G1526 | A1464 | G1402 | U1340 | U1281 | A1219 | C1161 | U1098 | G1025 |
| A1983 | C1921 | U1861 | U1647 | C1587 | G1527 | A1465 | A1403 | C1341 | A1282 | G1220 | A1162 | U1099 | U1026 |
| G1984 | C1922 | G1862 | C1648 | U1588 | C1528 | G1466 | G1404 | A1342 | U1283 | C1221 | A1163 | G1101 | G1027 |
| A1985 | G1923 | U1863 | C1649 | C1589 | G1529 | A1467 | U1405 | G1343 | A1284 | A1222 | U1164 | G1102 | G1028 |
| G1986 | G1924 | C1864 | U1650 | C1590 | G1530 | C1468 | A1406 | U1344 | A1285 | G1223 | C1165 | G1103 | C1040 |
| A1987 | G1925 | A1865 | U1651 | U1591 | C1531 | U1469 | A1407 | G1346 | G1286 | C1224 | C1167 | U1104 | U1042 |
| C1991 | U1926 | U1866 | C1652 | G1593 | C1532 | U1470 | G1408 | U1347 | G1287 | G1225 | A1168 | C1106 | A1043 |
| C1992 | G1927 | A1867 | U1653 | G1594 | G1533 | C1472 | A1410 | G1348 | C1288 | C1226 | U1169 | U1107 | A1044 |
| A1993 | A1928 | C1868 | U1654 | A1595 | G1534 | U1473 | U1411 | A1350 | U1290 | U1227 | A1170 | A1108 | C1045 |
| C1994 | U1929 | U1869 | C1656 | G1596 | C1537 | G1474 | G1412 | A1351 | C1291 | C1228 | G1171 | A1109 | A1046 |
| U1995 | G1931 | A1871 | A1657 | C1597 | G1538 | C1475 | C1413 | G1352 | A1292 | G1229 | U1172 | G1110 | A1047 |
| C1996 | U1932 | A1872 | U1658 | U1598 | U1539 | U1476 | U1414 | C1353 | A1293 | U1230 | G1173 | A1111 | C1048 |
| U1997 | A1933 | G1873 | A1659 | A1599 | G1540 | U1477 | G1415 | U1354 | U1294 | U1231 | G1174 | U1112 | C1049 |
| G1998 | C1934 | A1874 | A1660 | U1601 | G1541 | C1478 | A1416 | U1355 | U1295 | U1232 | A1175 | C1113 | C1050 |
| A1999 | U1935 | A1875 | U1661 | U1602 | G1542 | U1479 | C1417 | G1356 | C1296 | G1233 | A1176 | C1114 | C1051 |
| A2000 | G1936 | G1876 | U1662 | G1603 | U1543 | A1480 | U1418 | U1357 | A1297 | G1234 | A1177 | A1116 | A1052 |
| G2001 | C1940 | C1877 | A1663 | A1604 | A1544 | G1481 | U1419 | G1358 | U1298 | A1235 | A1178 | A1117 | G1053 |
| A2003 | C1941 | U1879 | A1664 | G1605 | C1545 | U1482 | G1420 | A1359 | U1299 | A1236 | G1179 | G1118 | G1054 |
| C2007 | G1942 | G1880 | C1665 | A1606 | A1546 | C1483 | A1421 | U1361 | C1300 | G1237 | A1181 | G1119 | G1055 |
| G2008 | A1943 | A1881 | C1666 | U1607 | C1547 | A1484 | G1422 | A1362 | C1301 | A1238 | A1182 | C1120 | A1057 |
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| C2010 | A1945 | A1883 | U1668 | U1609 | A1549 | U1486 | A1424 | U1364 | C1303 | G1240 | U1184 | A1122 | C1059 |
| A2011 | C1946 | C1884 | U1669 | G1610 | A1550 | C1487 | G1427 | G1365 | G1304 | C1241 | G1185 | G1123 | U1060 |
| G1947 | U1947 | U1885 | A1670 | G1611 | A1551 | U1488 | A1428 | G1366 | A1305 | G1242 | A1186 | A1124 | C1061 |
| C1948 | A1949 | U1886 | U1671 | G1612 | U1552 | U1489 | U1429 | G1367 | A1306 | U1243 | U1187 | G1125 | G1062 |
| U2015 | G1950 | C1887 | C1673 | G1613 | U1553 | C1490 | A1430 | G1368 | G1307 | A1244 | C1188 | G1126 | G1063 |
| G2016 | C1952 | A1888 | U1674 | C1614 | G1554 | G1491 | A1431 | A1369 | A1309 | A1245 | G1189 | A1129 | U1066 |
| C2017 | G1953 | G1890 | C1675 | C1615 | A1555 | C1492 | C1434 | A1370 | A1310 | U1246 | A1190 | A1130 | A1067 |
| C2018 | G1954 | A1891 | A1677 | G1616 | C1556 | A1493 | A1435 | G1371 | G1311 | U1247 | G1191 | C1131 | C1068 |
| C2019 | G1955 | A1892 | U1678 | G1617 | G1557 | G1494 | U1436 | A1376 | G1312 | A1248 | C1192 | A1132 | A1069 |
| C2020 | G1956 | A1893 | G1679 | G1618 | A1558 | G1495 | G1437 | U1375 | G1313 | G1249 | G1193 | G1133 | G1070 |
| C2021 | U1956 | A1894 | A1680 | G1619 | U1559 | U1496 | U1438 | U1376 | A1314 | C1251 | A1194 | C1134 | G1071 |
| G2022 | G1957 | A1895 | G1835 | G1620 | U1560 | U1497 | U1439 | U1377 | A1315 | U1250 | U1195 | G1135 | G1072 |
| U2023 | A1958 | A1896 | C1836 | A1622 | U1562 | A1499 | A1440 | G1378 | C1316 | A1252 | G1196 | C1136 | C1073 |
| A2024 | G1959 | A1897 | G1837 | C1623 | C1563 | A1500 | A1441 | U1501 | C1317 | C1253 | A1197 | A1137 | G1074 |
| C1960 | C1960 | C1898 | G1837 | C1624 | C1564 | U1502 | A1442 | G1379 | U1318 | U1254 | C1198 | U1138 | U1075 |
| U2027 | A1961 | U1899 | A1838 | G1625 | U1565 | G1503 | A1443 | U1380 | U1319 | G1255 | A1200 | A1139 | U1076 |
| U2028 | A1962 | U1900 | G1839 | U1626 | U1566 | G1504 | A1444 | G1381 | G1320 | G1256 | A1199 | A1138 | U1077 |
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| A2033 | A1903 | A1903 | U1842 | A1629 | A1569 | U1506 | A1446 | C1384 | A1323 | C1258 | C1079 | C1142 | G1080 |
| G2034 | G1966 | A1904 | G1843 | G1630 | C1570 | C1507 | C1447 | A1385 | G1324 | U1259 | A1203 |       |       |

|       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |       |
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| G2800 | A2801 | U2802 | G2803 | U2804 | G2805 | G2806 | A2807 | G2808 | U2809 | G2810 | A2811 | G2812 | C2813 | A2814 | G2815 | A2816 | U2817 | G2818 | C2819 | U2820 | G2821 | G2822 | G2823 | G2824 | U2825 | U2826 | A2828 | A2829 | G2830 | A2831 | A2832 | G2833 | G2834 | U2835 | G2836 | C2837 | C2838 | A2839 | G2840 | G2841 | C2842 | G2843 | U2844 | U2845 | C2846 | G2847 | U2848 | U2849 | U2852 | U2853 | C2854 | G2855 | U2856 | C2857 | U2858 | U2859 | C2862 | A2863 |       |
| G2740 | C2741 | G2742 | G2743 | G2744 | G2745 | A2746 | U2747 | A2748 | U2749 | G2750 | A2751 | G2752 | G2753 | U2754 | U2755 | A2756 | U2757 | G2758 | G2759 | A2760 | G2761 | U2762 | C2763 | G2764 | C2765 | A2766 | A2767 | G2768 | A2769 | G2770 | C2771 | U2772 | G2773 | U2774 | U2775 | A2776 | U2777 | G2778 | G2779 | A2780 | C2781 | G2782 | G2783 | A2784 | U2785 | U2786 | G2787 | U2788 | U2789 | U2790 | U2791 | G2792 | G2793 | G2794 | U2795 | G2796 | U2797 | U2798 | U2799 |
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| U2099 | A2100 | A2101 | A2102 | A2103 | A2104 | C2105 | A2106 | C2107 | A2108 | U2109 | G2110 | A2111 | C2112 | U2113 | U2114 | U2115 | U2116 | C2117 | U2118 | U2119 | A2120 | U2121 | U2122 | G2123 | G2124 | U2125 | A2126 | A2127 | C2128 | A2129 | G2130 | G2131 | U2132 | U2133 | G2134 | U2135 | A2136 | U2137 | A2138 | G2139 | A2140 | G2141 | U2142 | C2143 | U2144 | G2145 | A2146 | C2147 | A2148 | C2149 | C2150 | U2151 | G2152 | C2153 | G2154 | C2155 | U2156 | G2157 | U2158 |
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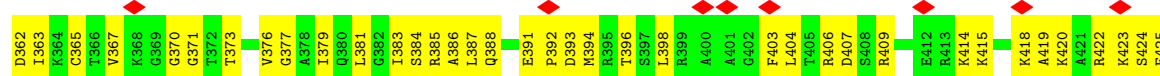
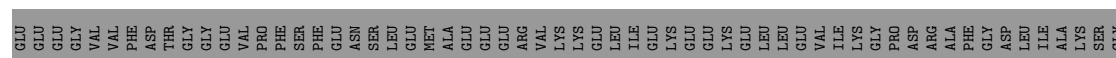
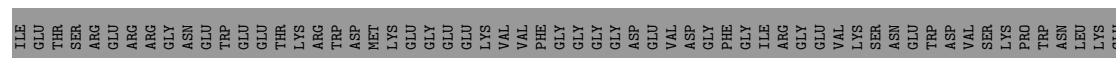
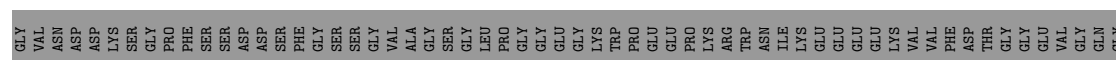
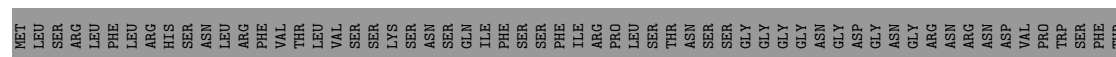




• Molecule 46: Ribosomal protein S7, mitochondrial

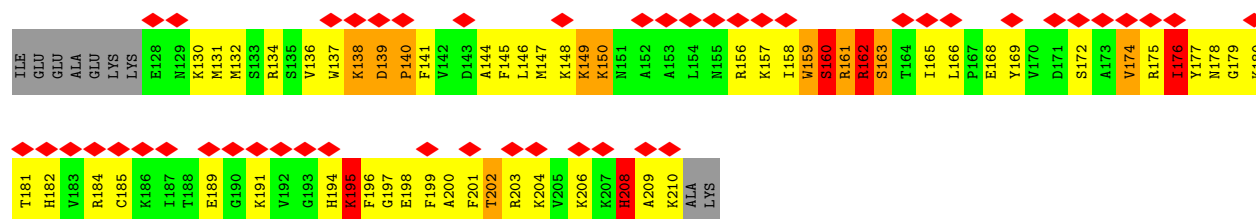


• Molecule 47: 30S ribosomal protein S9, mitochondrial

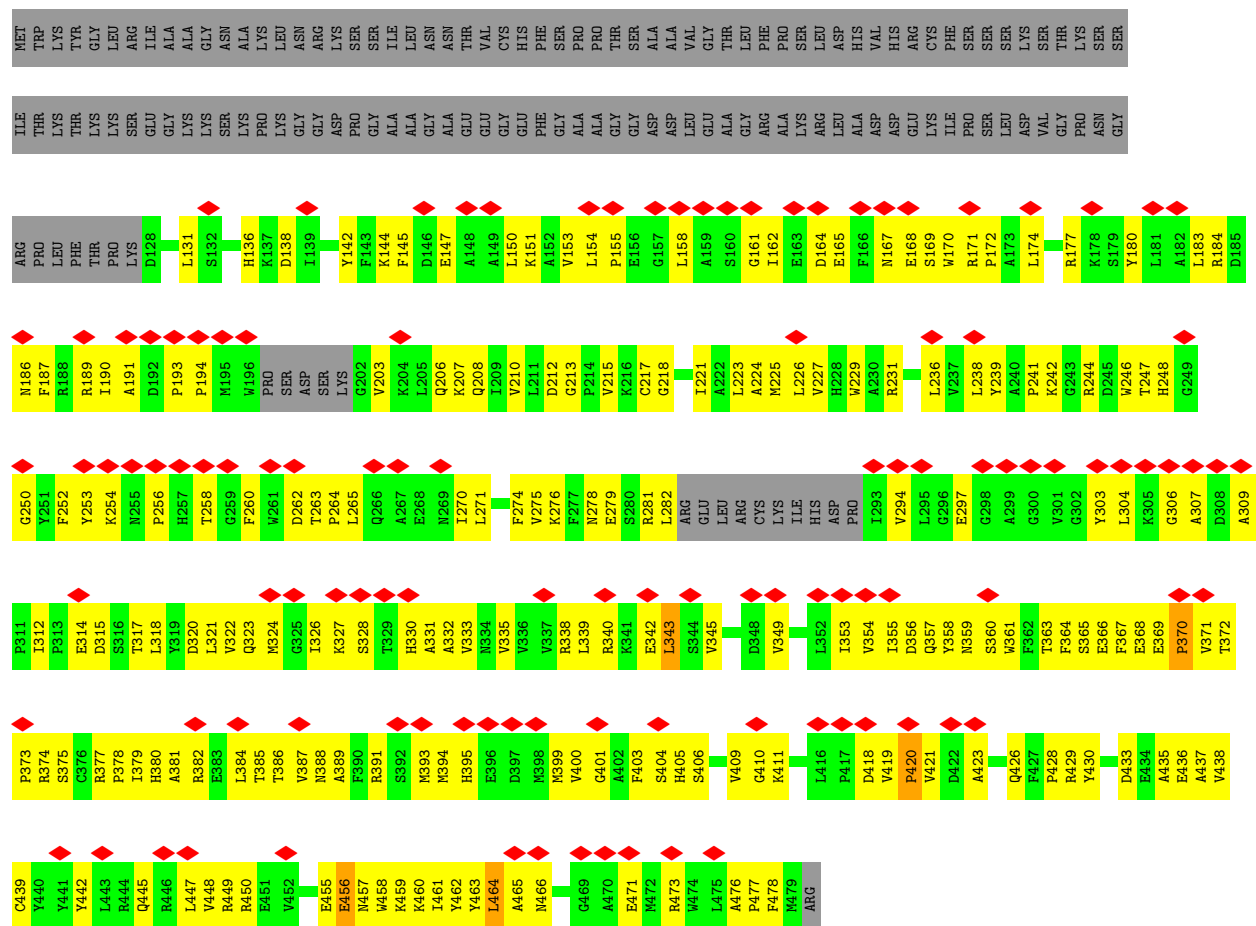


• Molecule 48: 40S ribosomal protein S10, mitochondrial

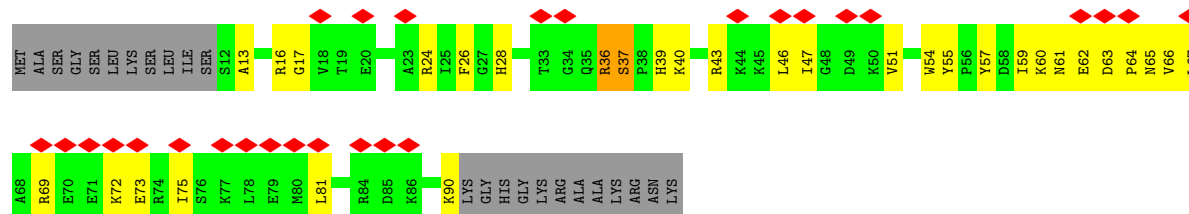




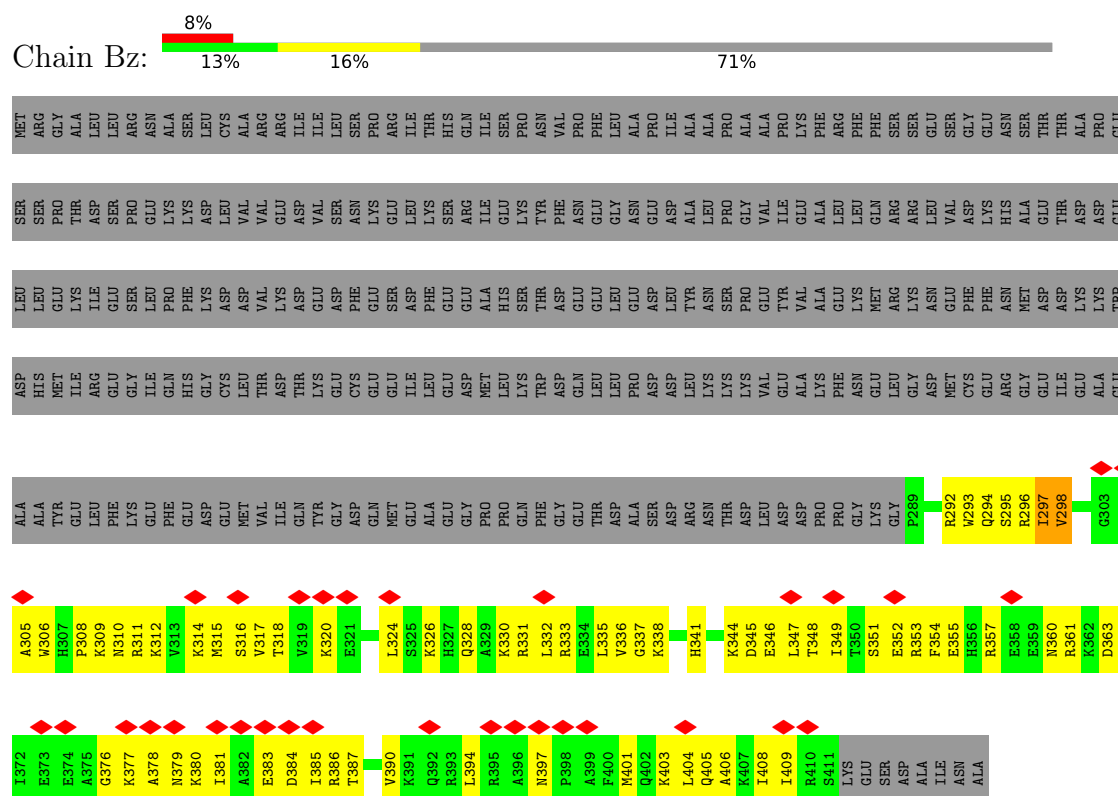
• Molecule 52: Mitochondrial 28S ribosomal protein S29-like protein



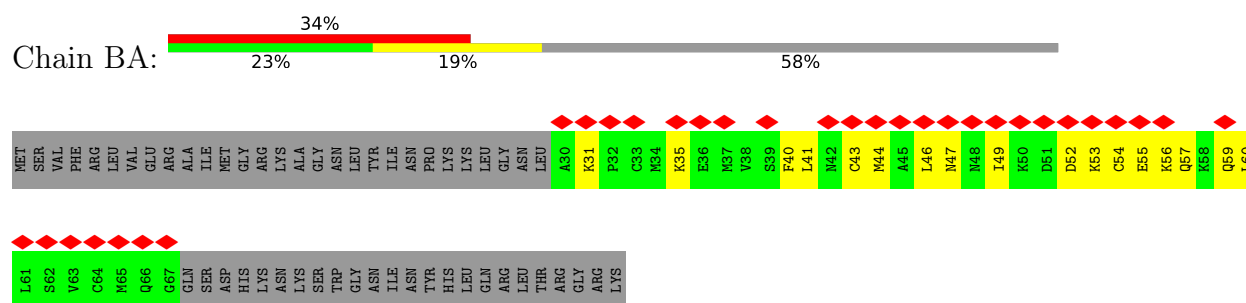
• Molecule 53: 37S ribosomal protein S27



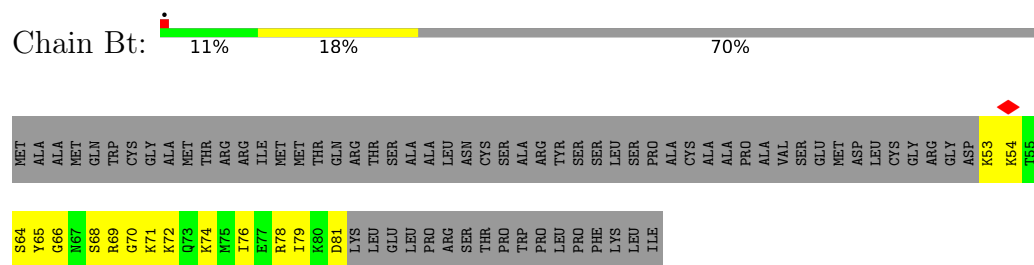
• Molecule 54: AT3G18240 protein



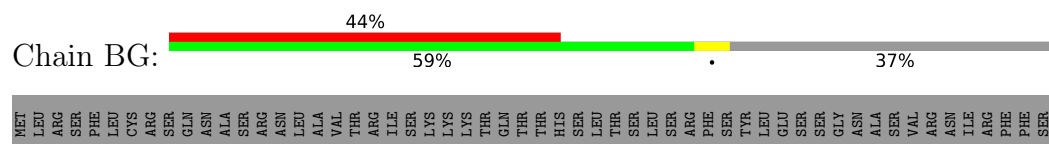
• Molecule 55: CX9C domain-containing protein



• Molecule 56: 30S ribosomal protein S31, mitochondrial

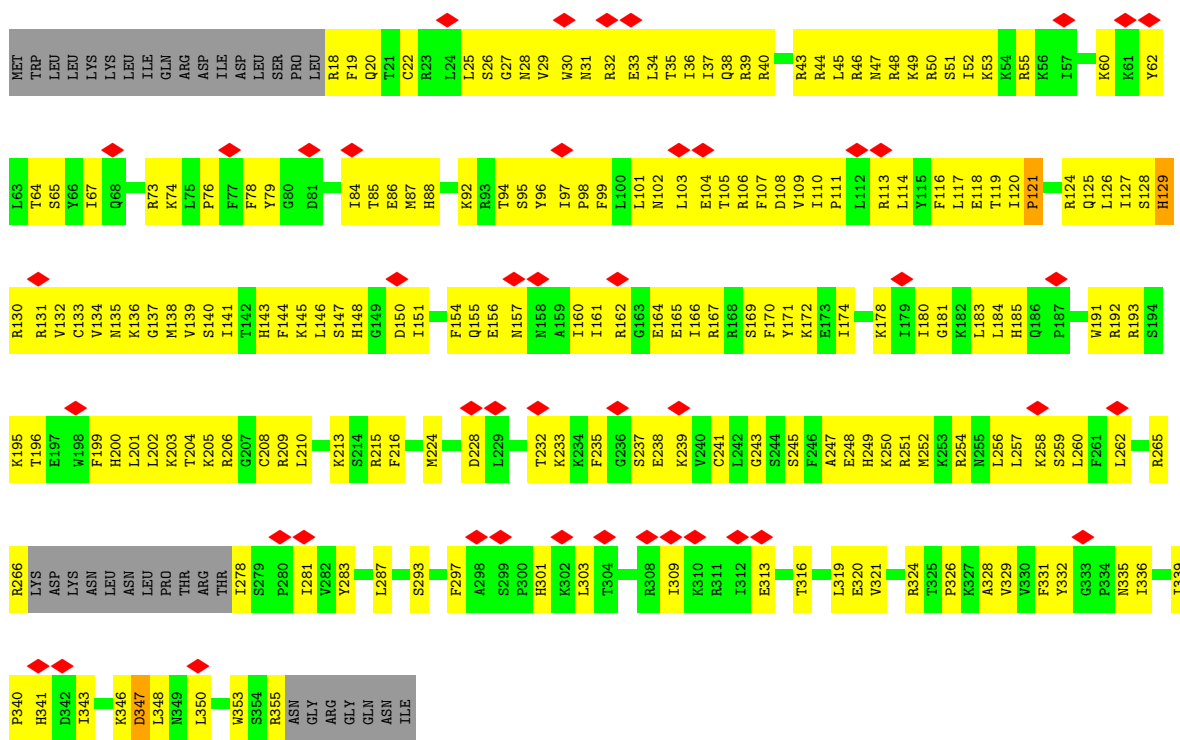


• Molecule 57: Pentatricopeptide repeat-containing protein At3g02650, mitochondrial

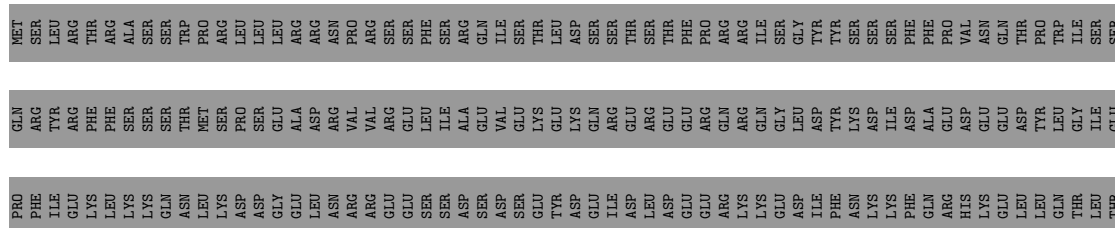


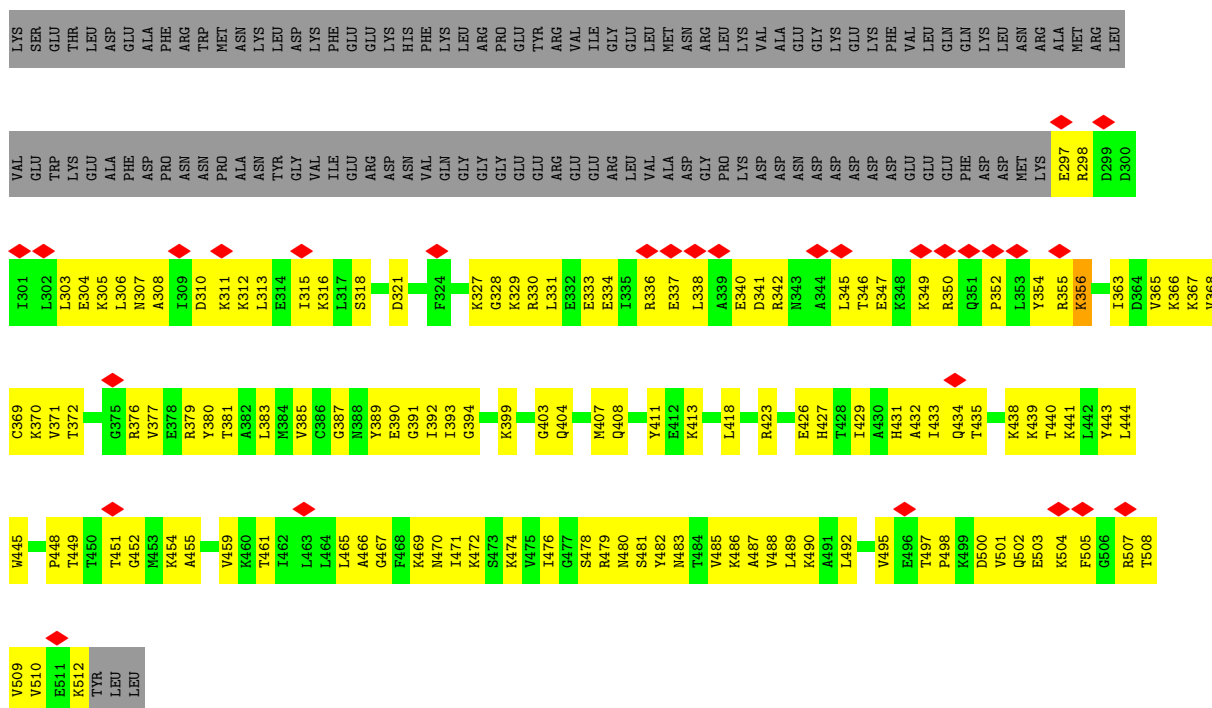


- Molecule 61: Ribosomal protein S4, mitochondrial

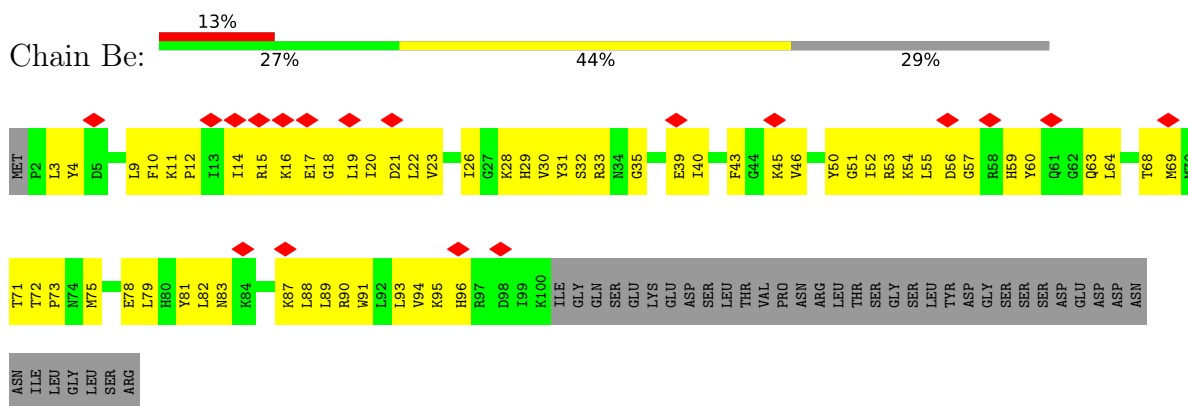


- Molecule 62: At1g64880

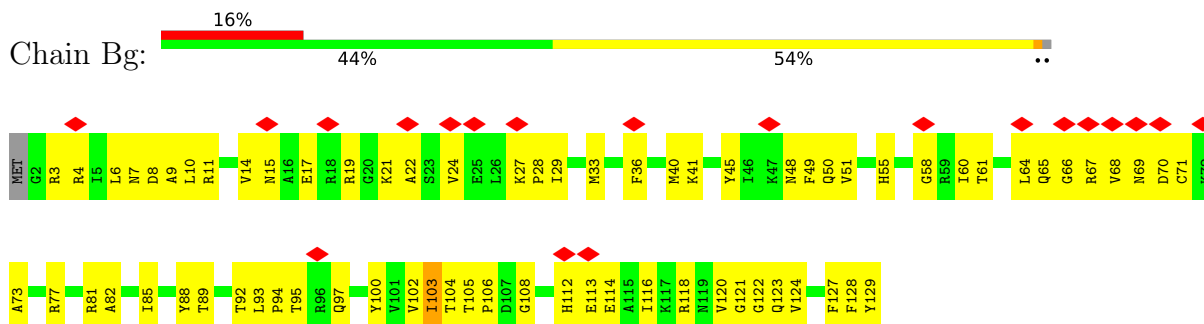




- Molecule 63: Translation elongation factor EF1B/ribosomal protein S6 family protein

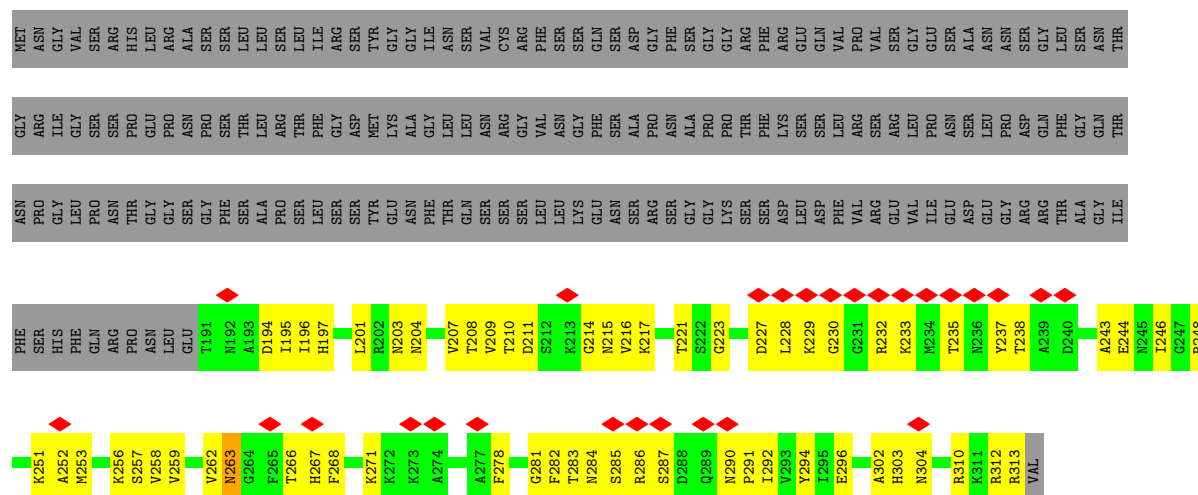


- Molecule 64: 40S ribosomal protein S15a-5

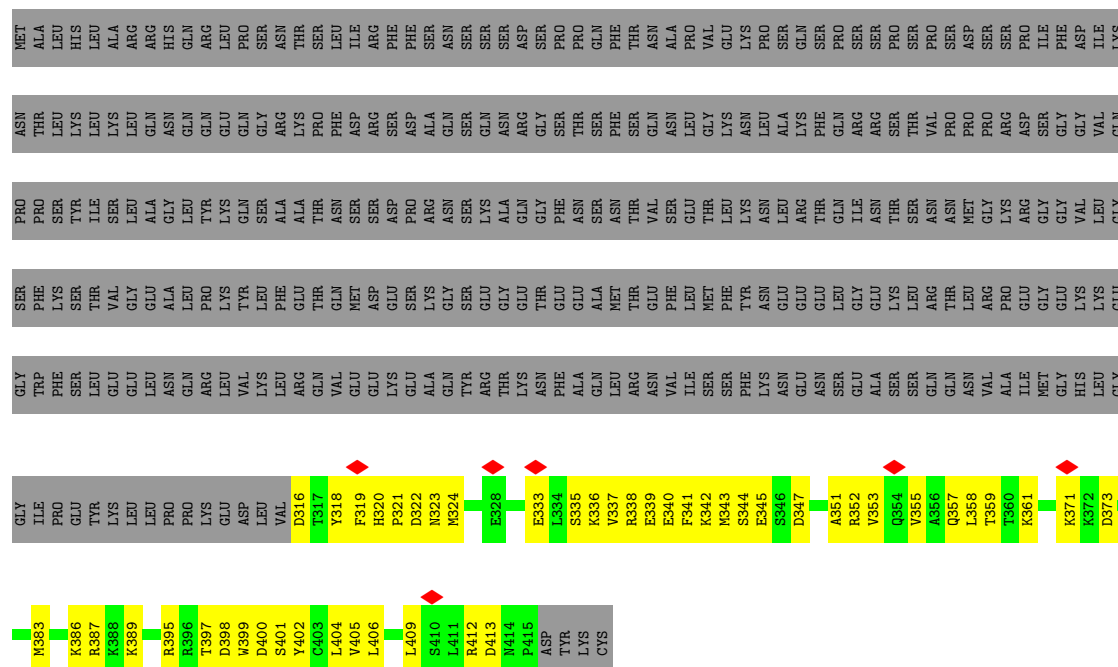


- Molecule 65: Probable ribosomal protein S11, mitochondrial

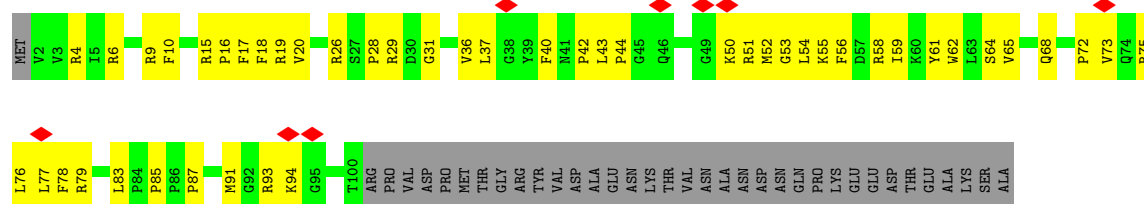




• Molecule 66: At1g15810/F7H2\_23

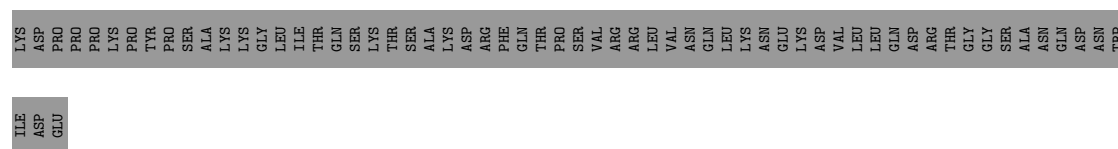


• Molecule 67: 30S ribosomal protein S16-2, chloroplastic/mitochondrial

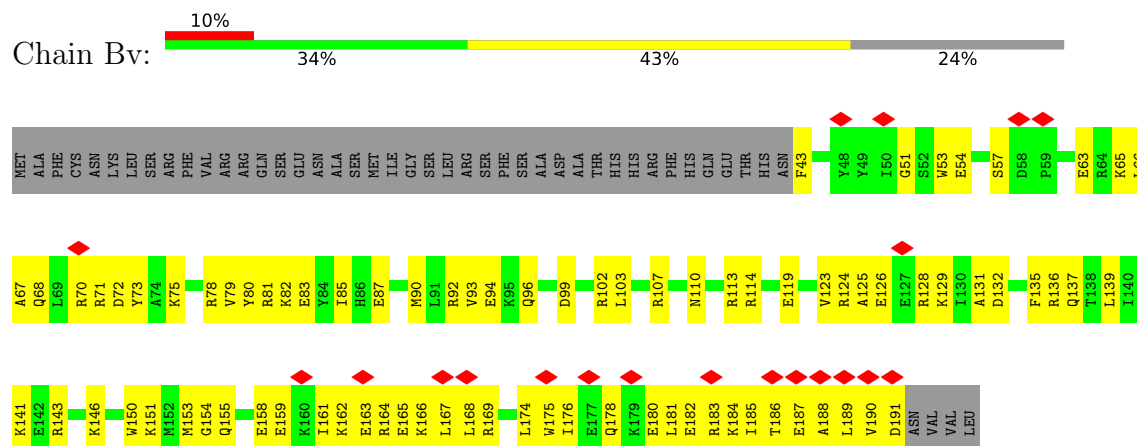


• Molecule 68: Nucleic acid-binding, OB-fold-like protein

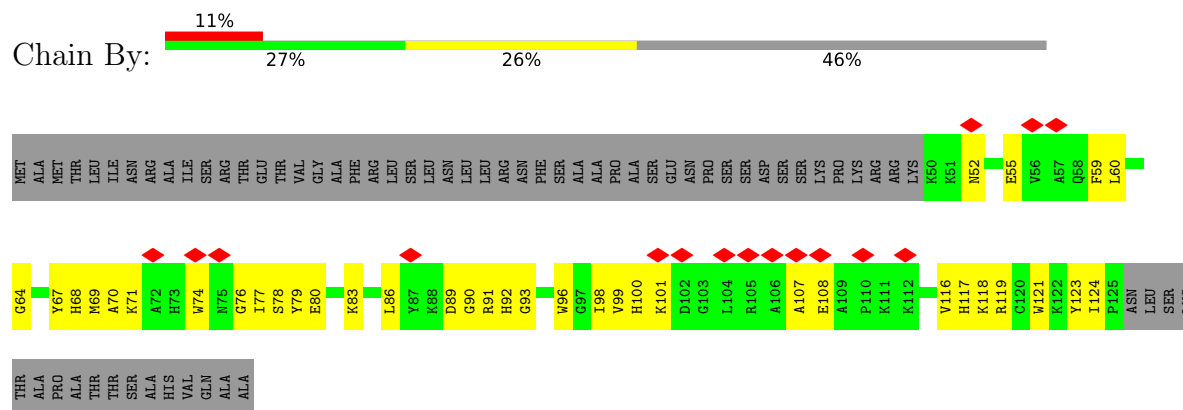




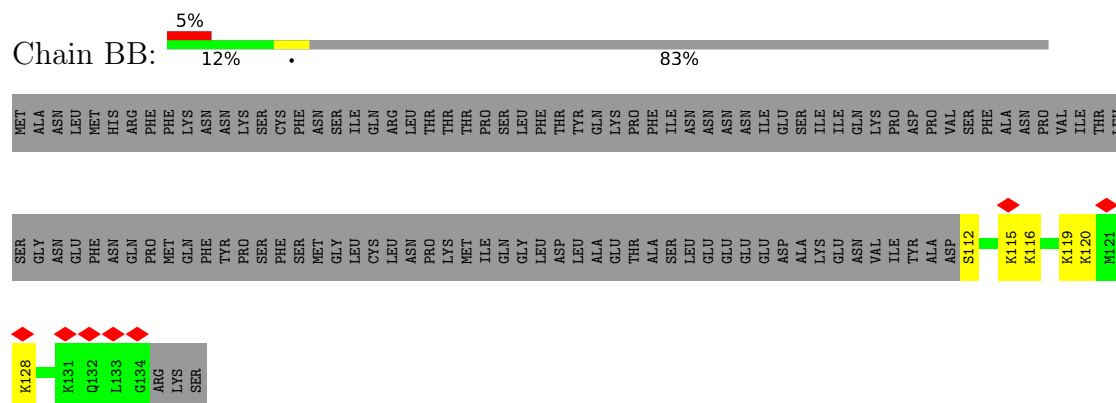
• Molecule 72: AT5g49210/K21P3\_8



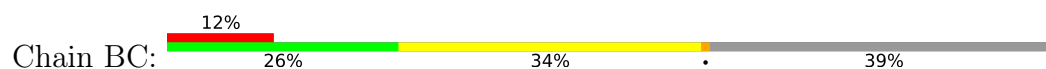
• Molecule 73: 28S ribosomal S34 protein

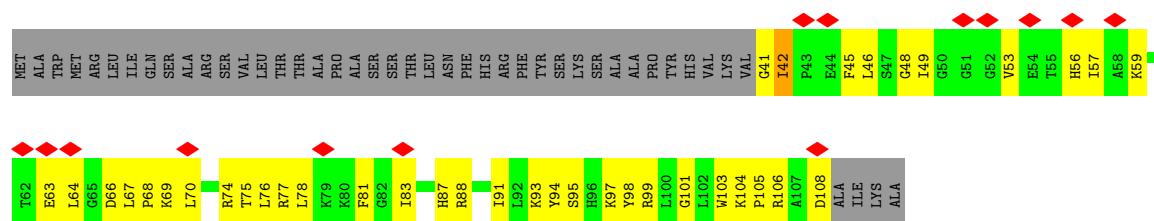


• Molecule 74: mS38

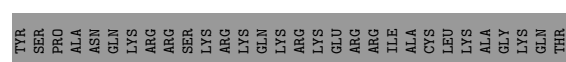
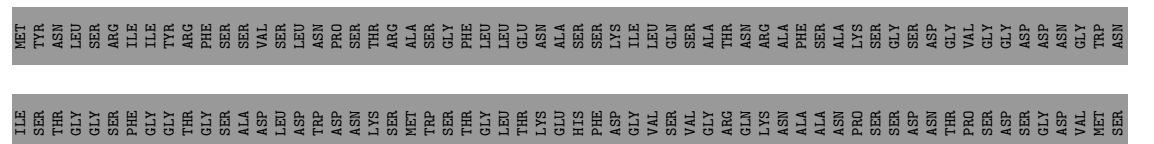
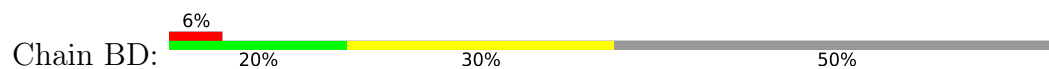


• Molecule 75: At5g26800

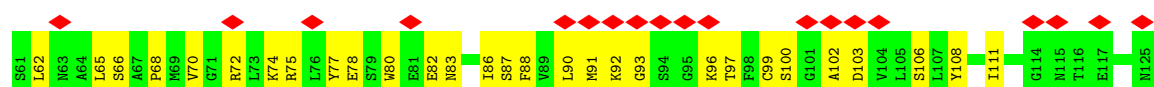
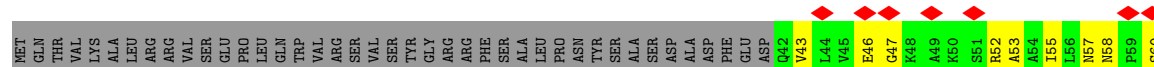


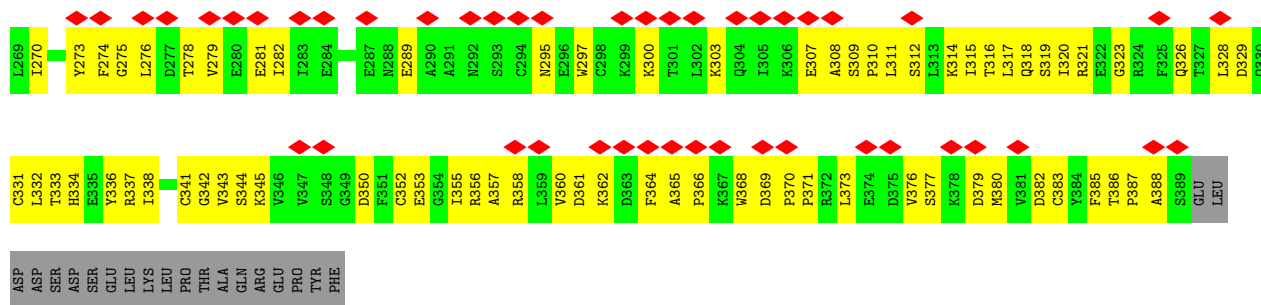


• Molecule 76: Gb|AAC32909.1

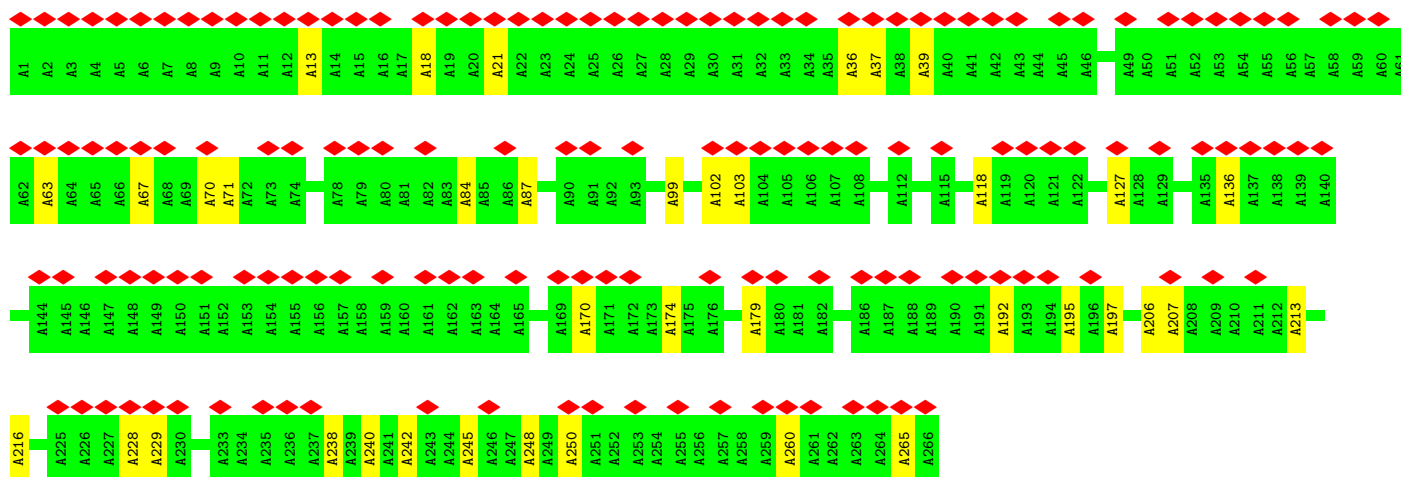
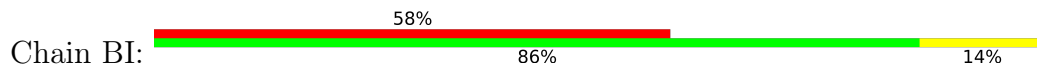


• Molecule 77: 3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial

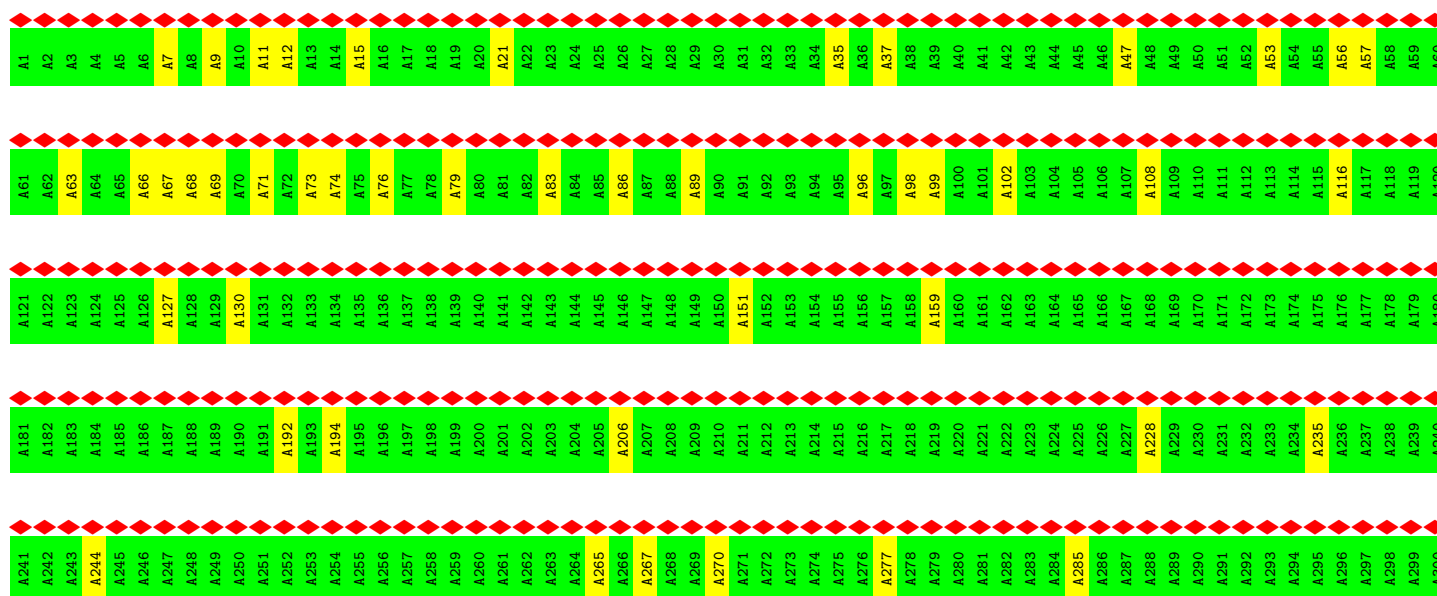
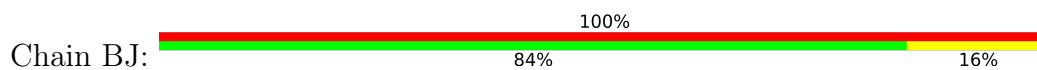




• Molecule 78: rPPR\*

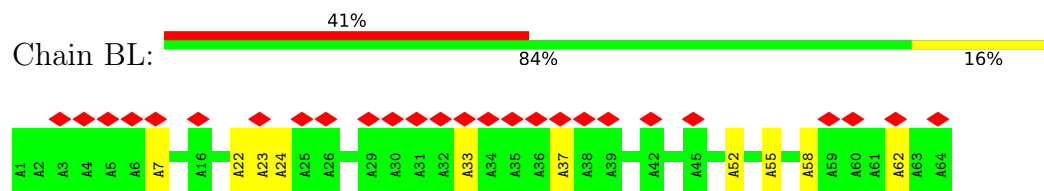


• Molecule 79: rPPR\*

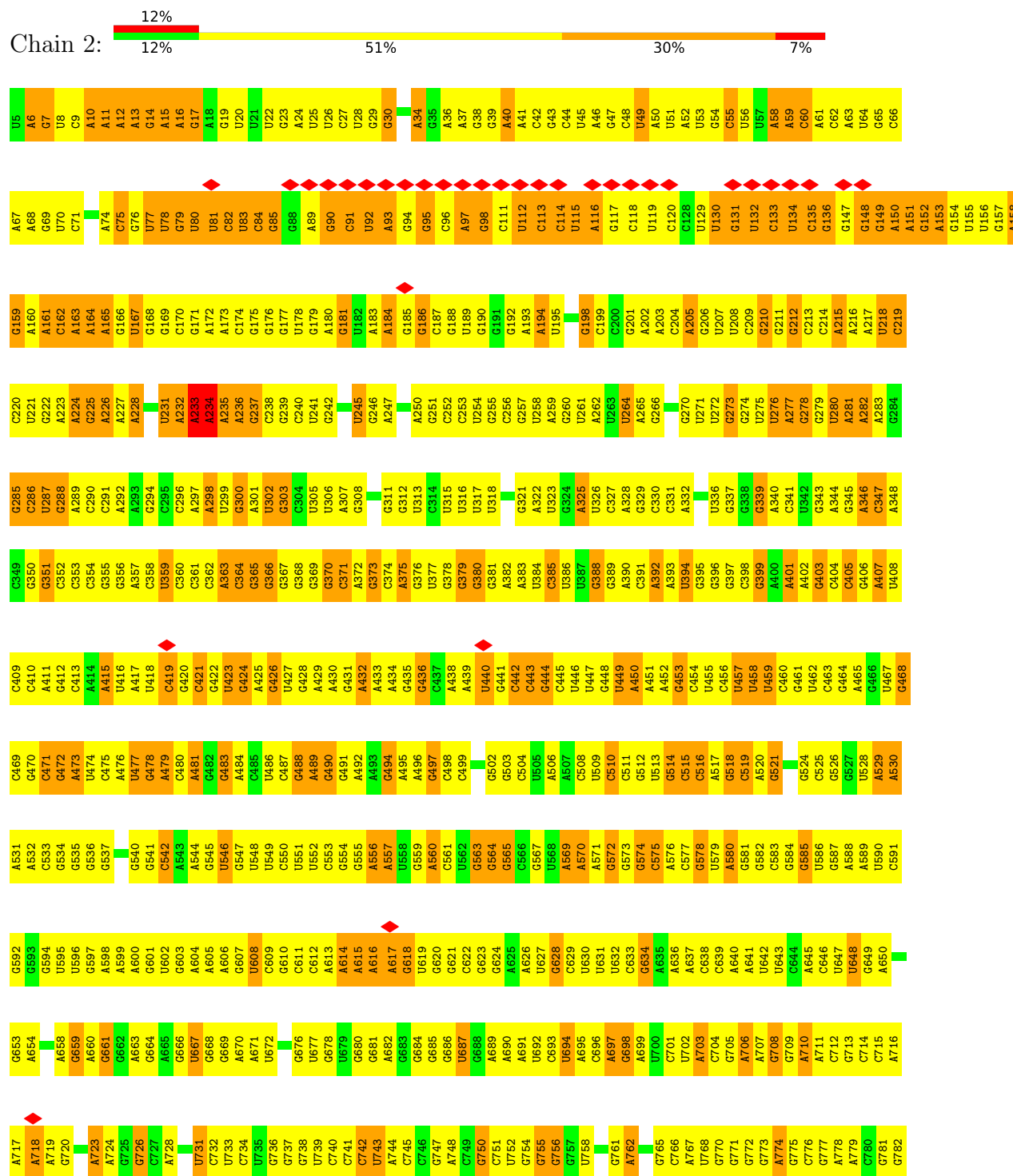




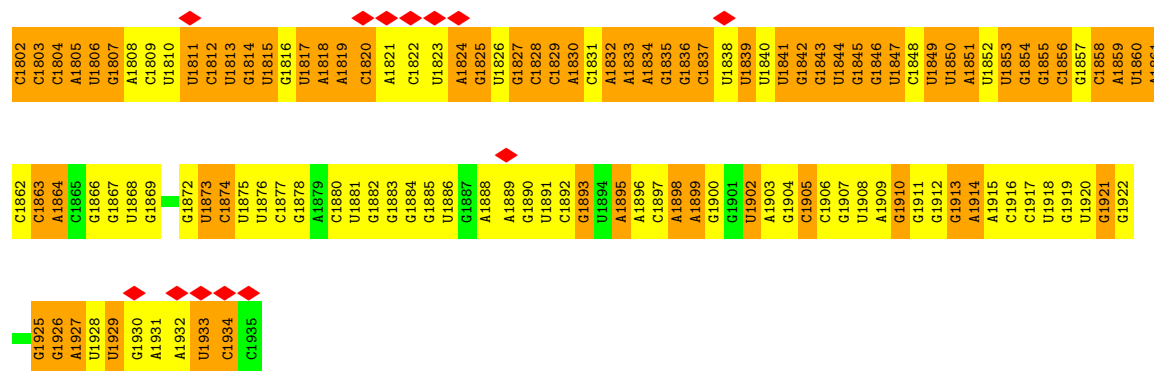
- Molecule 84: UNK-1



- Molecule 85: RNA (1743-MER)

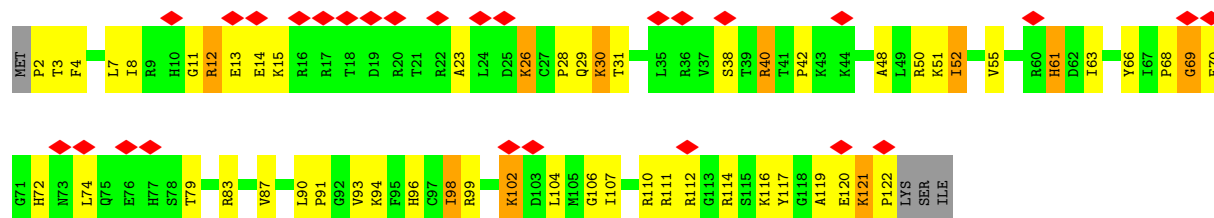








- Molecule 89: Ribosomal protein S12, mitochondrial



## 4 Experimental information

| Property                             | Value                                   | Source    |
|--------------------------------------|-----------------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                         | Depositor |
| Imposed symmetry                     | POINT, Not provided                     |           |
| Number of particles used             | 65280                                   | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF                       | Depositor |
| CTF correction method                | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope                           | FEI TALOS ARCTICA                       | Depositor |
| Voltage (kV)                         | 200                                     | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 3                                       | Depositor |
| Minimum defocus (nm)                 | Not provided                            |           |
| Maximum defocus (nm)                 | Not provided                            |           |
| Magnification                        | Not provided                            |           |
| Image detector                       | FEI FALCON III (4k x 4k)                | Depositor |
| Maximum map value                    | 0.196                                   | Depositor |
| Minimum map value                    | -0.082                                  | Depositor |
| Average map value                    | -0.000                                  | Depositor |
| Map value standard deviation         | 0.011                                   | Depositor |
| Recommended contour level            | 0.035                                   | Depositor |
| Map size (Å)                         | 484.0, 484.0, 484.0                     | wwPDB     |
| Map dimensions                       | 400, 400, 400                           | wwPDB     |
| Map angles (°)                       | 90.0, 90.0, 90.0                        | wwPDB     |
| Pixel spacing (Å)                    | 1.21, 1.21, 1.21                        | Depositor |

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths |             | Bond angles |               |
|-----|-------|--------------|-------------|-------------|---------------|
|     |       | RMSZ         | $\# Z  > 5$ | RMSZ        | $\# Z  > 5$   |
| 1   | Aa    | 0.54         | 0/764       | 0.84        | 1/1020 (0.1%) |
| 2   | Ab    | 0.43         | 0/1165      | 0.58        | 0/1554        |
| 3   | Ac    | 0.48         | 0/1710      | 0.68        | 1/2294 (0.0%) |
| 4   | AD    | 0.42         | 0/518       | 0.64        | 0/686         |
| 5   | Ad    | 0.48         | 0/1680      | 0.66        | 0/2267        |
| 6   | Ae    | 0.36         | 0/1198      | 0.69        | 0/1620        |
| 7   | Af    | 0.27         | 0/815       | 0.57        | 0/1091        |
| 8   | Ag    | 0.33         | 0/413       | 0.64        | 0/557         |
| 9   | Ai    | 0.34         | 0/1081      | 0.59        | 0/1467        |
| 10  | Aj    | 0.41         | 0/1294      | 0.62        | 0/1738        |
| 11  | Ak    | 0.41         | 0/972       | 0.60        | 0/1300        |
| 12  | Al    | 0.41         | 0/1433      | 0.64        | 0/1914        |
| 13  | Am    | 0.41         | 0/1135      | 0.70        | 1/1518 (0.1%) |
| 14  | An    | 0.54         | 0/1159      | 0.81        | 0/1556        |
| 15  | Ao    | 0.34         | 0/849       | 0.59        | 0/1141        |
| 16  | Ap    | 0.45         | 0/947       | 0.68        | 0/1268        |
| 17  | Aq    | 0.44         | 0/902       | 0.64        | 0/1195        |
| 18  | Ar    | 0.40         | 0/1124      | 0.68        | 0/1508        |
| 19  | As    | 0.47         | 0/947       | 0.67        | 0/1273        |
| 20  | At    | 0.44         | 0/854       | 0.60        | 0/1145        |
| 21  | Au    | 0.58         | 0/1133      | 0.92        | 2/1527 (0.1%) |
| 22  | Av    | 0.38         | 0/1546      | 0.66        | 0/2091        |
| 23  | Aw    | 0.48         | 0/620       | 0.59        | 0/829         |
| 24  | Ax    | 0.44         | 0/826       | 0.56        | 0/1105        |
| 25  | Ay    | 0.51         | 0/962       | 0.79        | 3/1290 (0.2%) |
| 26  | AA    | 0.50         | 0/303       | 0.93        | 0/400         |
| 27  | AB    | 0.47         | 0/326       | 0.72        | 0/433         |
| 28  | AC    | 0.40         | 0/441       | 0.56        | 0/584         |
| 29  | AE    | 0.34         | 0/300       | 0.54        | 0/394         |
| 30  | AF    | 0.41         | 0/674       | 0.72        | 0/908         |
| 31  | AG    | 0.46         | 0/500       | 0.72        | 0/677         |
| 32  | AH    | 0.38         | 0/894       | 0.60        | 0/1205        |
| 33  | AI    | 0.32         | 0/1765      | 0.59        | 0/2388        |
| 34  | AJ    | 0.36         | 0/639       | 0.67        | 0/862         |

| Mol | Chain | Bond lengths |              | Bond angles |                 |
|-----|-------|--------------|--------------|-------------|-----------------|
|     |       | RMSZ         | # Z  >5      | RMSZ        | # Z  >5         |
| 35  | AK    | 0.37         | 0/744        | 0.63        | 1/984 (0.1%)    |
| 36  | AL    | 0.39         | 0/407        | 0.65        | 0/549           |
| 37  | AM    | 0.34         | 0/667        | 0.54        | 0/899           |
| 38  | AN    | 0.34         | 0/667        | 0.54        | 0/877           |
| 39  | AO    | 0.32         | 0/3654       | 0.60        | 2/4927 (0.0%)   |
| 40  | AP    | 0.28         | 0/3344       | 0.65        | 3/4680 (0.1%)   |
| 41  | AQ    | 0.31         | 0/2947       | 0.57        | 0/3942          |
| 42  | AR    | 0.24         | 0/144        | 0.48        | 0/200           |
| 43  | 1     | 0.46         | 0/68131      | 0.51        | 1/106225 (0.0%) |
| 44  | 3     | 0.38         | 0/2810       | 0.58        | 3/4378 (0.1%)   |
| 45  | Bb    | 0.35         | 0/2346       | 0.62        | 0/3146          |
| 46  | Bf    | 0.26         | 0/1121       | 0.54        | 0/1501          |
| 47  | Bh    | 0.29         | 0/995        | 0.55        | 0/1336          |
| 48  | Bi    | 0.34         | 0/878        | 0.68        | 0/1175          |
| 49  | Bl    | 0.32         | 0/738        | 0.76        | 0/987           |
| 50  | Bm    | 0.31         | 0/807        | 0.60        | 0/1072          |
| 51  | Br    | 0.94         | 1/700 (0.1%) | 1.72        | 12/932 (1.3%)   |
| 52  | Bw    | 0.27         | 0/2793       | 0.65        | 0/3785          |
| 53  | Bx    | 0.34         | 0/653        | 0.63        | 0/873           |
| 54  | Bz    | 0.28         | 0/1027       | 0.52        | 0/1371          |
| 55  | BA    | 0.27         | 0/294        | 0.58        | 0/388           |
| 56  | Bt    | 0.26         | 0/240        | 0.59        | 0/307           |
| 57  | BG    | 0.27         | 0/1794       | 0.69        | 9/2495 (0.4%)   |
| 58  | BP    | 0.19         | 0/451        | 0.29        | 0/625           |
| 59  | BF    | 0.21         | 0/614        | 0.52        | 0/858           |
| 60  | Ba    | 0.44         | 0/1600       | 0.90        | 4/2162 (0.2%)   |
| 61  | Bc    | 0.32         | 0/2831       | 0.67        | 0/3795          |
| 62  | Bd    | 0.41         | 0/1755       | 0.65        | 0/2351          |
| 63  | Be    | 0.33         | 0/834        | 0.67        | 0/1115          |
| 64  | Bg    | 0.37         | 0/1059       | 0.68        | 0/1424          |
| 65  | Bj    | 0.31         | 0/967        | 0.55        | 0/1293          |
| 66  | Bn    | 0.34         | 0/826        | 0.56        | 0/1099          |
| 67  | Bo    | 0.36         | 0/800        | 0.69        | 0/1074          |
| 68  | Bp    | 0.34         | 0/647        | 0.58        | 0/868           |
| 69  | Bq    | 0.35         | 0/497        | 0.55        | 0/664           |
| 70  | Bs    | 0.29         | 0/542        | 0.53        | 0/716           |
| 71  | Bu    | 0.27         | 0/815        | 0.54        | 0/1091          |
| 72  | Bv    | 0.29         | 0/1294       | 0.55        | 0/1721          |
| 73  | By    | 0.27         | 0/639        | 0.53        | 0/860           |
| 74  | BB    | 0.36         | 0/204        | 0.46        | 0/260           |
| 75  | BC    | 0.27         | 0/556        | 0.56        | 0/745           |
| 76  | BD    | 0.32         | 0/1805       | 0.61        | 0/2409          |
| 77  | BE    | 0.28         | 0/2751       | 0.56        | 0/3723          |

| Mol | Chain | Bond lengths |                   | Bond angles |                   |
|-----|-------|--------------|-------------------|-------------|-------------------|
|     |       | RMSZ         | # Z  >5           | RMSZ        | # Z  >5           |
| 78  | BI    | 0.18         | 0/1329            | 0.42        | 0/1859            |
| 79  | BJ    | 0.18         | 0/1744            | 0.43        | 0/2440            |
| 80  | BH    | 0.25         | 0/1022            | 0.68        | 6/1425 (0.4%)     |
| 81  | BN    | 0.23         | 0/344             | 0.43        | 0/480             |
| 82  | BM    | 0.21         | 0/394             | 0.46        | 0/550             |
| 83  | BO    | 0.18         | 0/149             | 0.28        | 0/207             |
| 84  | BL    | 0.21         | 0/319             | 0.42        | 0/445             |
| 85  | 2     | 0.99         | 181/41845 (0.4%)  | 0.91        | 229/65247 (0.4%)  |
| 86  | Az    | 1.11         | 0/669             | 1.46        | 11/898 (1.2%)     |
| 87  | Ah    | 0.97         | 1/1117 (0.1%)     | 1.46        | 8/1505 (0.5%)     |
| 88  | BK    | 1.15         | 0/1579            | 1.61        | 9/2209 (0.4%)     |
| 89  | Bk    | 0.91         | 0/985             | 1.33        | 6/1315 (0.5%)     |
| All | All   | 0.60         | 183/202773 (0.1%) | 0.70        | 312/297267 (0.1%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 18  | Ar    | 0                   | 2                   |
| 20  | At    | 0                   | 1                   |
| 21  | Au    | 0                   | 1                   |
| 24  | Ax    | 0                   | 1                   |
| 26  | AA    | 0                   | 1                   |
| 27  | AB    | 0                   | 1                   |
| 33  | AI    | 0                   | 1                   |
| 37  | AM    | 0                   | 2                   |
| 39  | AO    | 0                   | 2                   |
| 40  | AP    | 0                   | 3                   |
| 41  | AQ    | 0                   | 1                   |
| 48  | Bi    | 0                   | 1                   |
| 49  | Bl    | 0                   | 1                   |
| 51  | Br    | 0                   | 2                   |
| 52  | Bw    | 0                   | 1                   |
| 61  | Bc    | 0                   | 1                   |
| 62  | Bd    | 0                   | 2                   |
| 65  | Bj    | 0                   | 1                   |
| 79  | BJ    | 0                   | 1                   |
| 85  | 2     | 5                   | 30                  |
| 87  | Ah    | 0                   | 2                   |
| All | All   | 5                   | 58                  |

The worst 5 of 183 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms | Z      | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 85  | 2     | 1391 | A    | O3'-P | -43.87 | 0.95        | 1.61     |
| 85  | 2     | 1402 | U    | O3'-P | -37.69 | 1.04        | 1.61     |
| 85  | 2     | 1450 | C    | O3'-P | 37.41  | 2.17        | 1.61     |
| 85  | 2     | 1385 | C    | O3'-P | -35.61 | 1.07        | 1.61     |
| 85  | 2     | 1379 | U    | O3'-P | -35.44 | 1.07        | 1.61     |

The worst 5 of 312 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms       | Z      | Observed(°) | Ideal(°) |
|-----|-------|------|------|-------------|--------|-------------|----------|
| 85  | 2     | 1445 | U    | O3'-P-O5'   | -40.52 | 43.22       | 104.00   |
| 85  | 2     | 1428 | G    | P-O3'-C3'   | 31.37  | 167.26      | 120.20   |
| 85  | 2     | 1451 | G    | O3'-P-O5'   | 29.65  | 148.48      | 104.00   |
| 85  | 2     | 1409 | G    | C2'-C3'-O3' | -29.48 | 69.48       | 113.70   |
| 85  | 2     | 1379 | U    | O5'-C5'-C4' | 28.92  | 154.89      | 111.50   |

All (5) chirality outliers are listed below:

| Mol | Chain | Res  | Type | Atom |
|-----|-------|------|------|------|
| 85  | 2     | 1165 | C    | C4'  |
| 85  | 2     | 1206 | G    | C3'  |
| 85  | 2     | 1404 | C    | C3'  |
| 85  | 2     | 1409 | G    | C4'  |
| 85  | 2     | 1410 | A    | C2'  |

5 of 58 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group   |
|-----|-------|-----|------|---------|
| 18  | Ar    | 164 | LEU  | Peptide |
| 18  | Ar    | 191 | ARG  | Peptide |
| 20  | At    | 102 | LYS  | Peptide |
| 21  | Au    | 132 | THR  | Peptide |
| 24  | Ax    | 57  | ASN  | Peptide |

## 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | Aa    | 753   | 0        | 794      | 53      | 0            |
| 2   | Ab    | 1144  | 0        | 1212     | 77      | 0            |
| 3   | Ac    | 1674  | 0        | 1722     | 121     | 0            |
| 4   | AD    | 506   | 0        | 554      | 28      | 0            |
| 5   | Ad    | 1649  | 0        | 1720     | 77      | 0            |
| 6   | Ae    | 1171  | 0        | 1171     | 111     | 0            |
| 7   | Af    | 797   | 0        | 827      | 52      | 0            |
| 8   | Ag    | 406   | 0        | 434      | 12      | 0            |
| 9   | Ai    | 1056  | 0        | 1088     | 68      | 0            |
| 10  | Aj    | 1267  | 0        | 1304     | 97      | 0            |
| 11  | Ak    | 962   | 0        | 1038     | 56      | 0            |
| 12  | Al    | 1407  | 0        | 1521     | 82      | 0            |
| 13  | Am    | 1111  | 0        | 1151     | 50      | 0            |
| 14  | An    | 1139  | 0        | 1178     | 64      | 0            |
| 15  | Ao    | 835   | 0        | 886      | 47      | 0            |
| 16  | Ap    | 935   | 0        | 1029     | 63      | 0            |
| 17  | Aq    | 888   | 0        | 924      | 71      | 0            |
| 18  | Ar    | 1106  | 0        | 1157     | 150     | 0            |
| 19  | As    | 937   | 0        | 1003     | 57      | 0            |
| 20  | At    | 840   | 0        | 907      | 49      | 0            |
| 21  | Au    | 1112  | 0        | 1167     | 120     | 0            |
| 22  | Av    | 1523  | 0        | 1606     | 127     | 0            |
| 23  | Aw    | 606   | 0        | 625      | 34      | 0            |
| 24  | Ax    | 809   | 0        | 813      | 40      | 0            |
| 25  | Ay    | 943   | 0        | 955      | 86      | 0            |
| 26  | AA    | 299   | 0        | 294      | 57      | 0            |
| 27  | AB    | 319   | 0        | 349      | 18      | 0            |
| 28  | AC    | 432   | 0        | 454      | 30      | 0            |
| 29  | AE    | 297   | 0        | 323      | 20      | 0            |
| 30  | AF    | 663   | 0        | 683      | 67      | 0            |
| 31  | AG    | 485   | 0        | 500      | 37      | 0            |
| 32  | AH    | 879   | 0        | 916      | 56      | 0            |
| 33  | AI    | 1714  | 0        | 1688     | 169     | 0            |
| 34  | AJ    | 632   | 0        | 645      | 95      | 0            |
| 35  | AK    | 732   | 0        | 770      | 44      | 0            |
| 36  | AL    | 400   | 0        | 417      | 56      | 0            |
| 37  | AM    | 651   | 0        | 690      | 28      | 0            |
| 38  | AN    | 664   | 0        | 722      | 27      | 0            |
| 39  | AO    | 3595  | 0        | 3655     | 280     | 0            |
| 40  | AP    | 3345  | 0        | 3344     | 110     | 0            |
| 41  | AQ    | 2900  | 0        | 2949     | 176     | 0            |
| 42  | AR    | 145   | 0        | 147      | 1       | 0            |
| 43  | 1     | 60842 | 0        | 30643    | 3474    | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 44  | 3     | 2513  | 0        | 1274     | 176     | 0            |
| 45  | Bb    | 2293  | 0        | 2313     | 122     | 0            |
| 46  | Bf    | 1106  | 0        | 1176     | 63      | 0            |
| 47  | Bh    | 975   | 0        | 1001     | 86      | 0            |
| 48  | Bi    | 857   | 0        | 911      | 89      | 0            |
| 49  | Bl    | 729   | 0        | 737      | 77      | 0            |
| 50  | Bm    | 794   | 0        | 835      | 74      | 0            |
| 51  | Br    | 685   | 0        | 715      | 153     | 0            |
| 52  | Bw    | 2722  | 0        | 2691     | 198     | 0            |
| 53  | Bx    | 641   | 0        | 670      | 35      | 0            |
| 54  | Bz    | 1010  | 0        | 1056     | 92      | 0            |
| 55  | BA    | 293   | 0        | 307      | 15      | 0            |
| 56  | Bt    | 239   | 0        | 270      | 19      | 0            |
| 57  | BG    | 1795  | 0        | 845      | 13      | 0            |
| 58  | BP    | 455   | 0        | 451      | 2       | 0            |
| 59  | BF    | 615   | 0        | 617      | 8       | 0            |
| 60  | Ba    | 1563  | 0        | 1578     | 86      | 0            |
| 61  | Bc    | 2772  | 0        | 2932     | 223     | 0            |
| 62  | Bd    | 1730  | 0        | 1810     | 146     | 0            |
| 63  | Be    | 819   | 0        | 869      | 62      | 0            |
| 64  | Bg    | 1042  | 0        | 1069     | 71      | 0            |
| 65  | Bj    | 955   | 0        | 996      | 85      | 0            |
| 66  | Bn    | 814   | 0        | 849      | 51      | 0            |
| 67  | Bo    | 780   | 0        | 805      | 62      | 0            |
| 68  | Bp    | 636   | 0        | 671      | 54      | 0            |
| 69  | Bq    | 492   | 0        | 522      | 21      | 0            |
| 70  | Bs    | 539   | 0        | 592      | 16      | 0            |
| 71  | Bu    | 800   | 0        | 833      | 41      | 0            |
| 72  | Bv    | 1278  | 0        | 1315     | 84      | 0            |
| 73  | By    | 619   | 0        | 629      | 48      | 0            |
| 74  | BB    | 203   | 0        | 246      | 5       | 0            |
| 75  | BC    | 544   | 0        | 590      | 41      | 0            |
| 76  | BD    | 1768  | 0        | 1737     | 143     | 0            |
| 77  | BE    | 2697  | 0        | 2691     | 157     | 0            |
| 78  | BI    | 1330  | 0        | 1332     | 34      | 0            |
| 79  | BJ    | 1745  | 0        | 1747     | 34      | 0            |
| 80  | BH    | 1023  | 0        | 478      | 3       | 0            |
| 81  | BN    | 345   | 0        | 347      | 11      | 0            |
| 82  | BM    | 395   | 0        | 397      | 5       | 0            |
| 83  | BO    | 150   | 0        | 152      | 1       | 0            |
| 84  | BL    | 320   | 0        | 322      | 9       | 0            |
| 85  | 2     | 37379 | 0        | 18835    | 2593    | 0            |

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| Mol | Chain | Non-H  | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 86  | Az    | 660    | 0        | 684      | 198     | 0            |
| 87  | Ah    | 1098   | 0        | 1133     | 75      | 0            |
| 88  | BK    | 1580   | 0        | 1579     | 136     | 0            |
| 89  | Bk    | 968    | 0        | 1019     | 119     | 0            |
| All | All   | 189336 | 0        | 140603   | 11005   | 0            |

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 34.

The worst 5 of 11005 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1             | Atom-2            | Interatomic distance (Å) | Clash overlap (Å) |
|--------------------|-------------------|--------------------------|-------------------|
| 51:Br:146:LEU:HD13 | 51:Br:150:LYS:CD  | 1.18                     | 1.62              |
| 87:Ah:121:TYR:CE1  | 87:Ah:126:TYR:CD1 | 1.84                     | 1.62              |
| 18:Ar:193:ILE:HD13 | 86:Az:90:LEU:CB   | 1.20                     | 1.61              |
| 18:Ar:193:ILE:CG2  | 86:Az:90:LEU:HD22 | 1.33                     | 1.55              |
| 87:Ah:121:TYR:CD1  | 87:Ah:126:TYR:HD1 | 1.24                     | 1.54              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 1   | Aa    | 94/349 (27%)  | 78 (83%)  | 14 (15%) | 2 (2%)   | 5           | 32  |
| 2   | Ab    | 153/214 (72%) | 129 (84%) | 24 (16%) | 0        | 100         | 100 |
| 3   | Ac    | 216/324 (67%) | 167 (77%) | 49 (23%) | 0        | 100         | 100 |
| 4   | AD    | 58/173 (34%)  | 49 (84%)  | 9 (16%)  | 0        | 100         | 100 |
| 5   | Ad    | 207/300 (69%) | 186 (90%) | 21 (10%) | 0        | 100         | 100 |
| 6   | Ae    | 142/185 (77%) | 114 (80%) | 28 (20%) | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |     |
|-----|-------|---------------|-----------|----------|----------|-------------|-----|
| 7   | Af    | 98/102 (96%)  | 80 (82%)  | 18 (18%) | 0        | 100         | 100 |
| 8   | Ag    | 49/221 (22%)  | 43 (88%)  | 6 (12%)  | 0        | 100         | 100 |
| 9   | Ai    | 136/155 (88%) | 120 (88%) | 16 (12%) | 0        | 100         | 100 |
| 10  | Aj    | 153/205 (75%) | 119 (78%) | 34 (22%) | 0        | 100         | 100 |
| 11  | Ak    | 125/173 (72%) | 102 (82%) | 23 (18%) | 0        | 100         | 100 |
| 12  | Al    | 176/281 (63%) | 145 (82%) | 31 (18%) | 0        | 100         | 100 |
| 13  | Am    | 140/179 (78%) | 122 (87%) | 18 (13%) | 0        | 100         | 100 |
| 14  | An    | 139/160 (87%) | 114 (82%) | 24 (17%) | 1 (1%)   | 18          | 53  |
| 15  | Ao    | 104/114 (91%) | 83 (80%)  | 21 (20%) | 0        | 100         | 100 |
| 16  | Ap    | 112/222 (50%) | 91 (81%)  | 21 (19%) | 0        | 100         | 100 |
| 17  | Aq    | 104/126 (82%) | 92 (88%)  | 12 (12%) | 0        | 100         | 100 |
| 18  | Ar    | 135/270 (50%) | 101 (75%) | 34 (25%) | 0        | 100         | 100 |
| 19  | As    | 119/269 (44%) | 106 (89%) | 13 (11%) | 0        | 100         | 100 |
| 20  | At    | 103/178 (58%) | 80 (78%)  | 23 (22%) | 0        | 100         | 100 |
| 21  | Au    | 138/159 (87%) | 97 (70%)  | 39 (28%) | 2 (1%)   | 9           | 38  |
| 22  | Av    | 194/249 (78%) | 166 (86%) | 28 (14%) | 0        | 100         | 100 |
| 23  | Aw    | 74/154 (48%)  | 63 (85%)  | 11 (15%) | 0        | 100         | 100 |
| 24  | Ax    | 97/212 (46%)  | 85 (88%)  | 12 (12%) | 0        | 100         | 100 |
| 25  | Ay    | 109/144 (76%) | 87 (80%)  | 22 (20%) | 0        | 100         | 100 |
| 26  | AA    | 35/76 (46%)   | 27 (77%)  | 8 (23%)  | 0        | 100         | 100 |
| 27  | AB    | 39/134 (29%)  | 27 (69%)  | 12 (31%) | 0        | 100         | 100 |
| 28  | AC    | 49/58 (84%)   | 43 (88%)  | 6 (12%)  | 0        | 100         | 100 |
| 29  | AE    | 34/103 (33%)  | 29 (85%)  | 5 (15%)  | 0        | 100         | 100 |
| 30  | AF    | 82/250 (33%)  | 74 (90%)  | 8 (10%)  | 0        | 100         | 100 |
| 31  | AG    | 59/94 (63%)   | 40 (68%)  | 18 (30%) | 1 (2%)   | 7           | 35  |
| 32  | AH    | 106/146 (73%) | 90 (85%)  | 16 (15%) | 0        | 100         | 100 |
| 33  | AI    | 205/233 (88%) | 161 (78%) | 44 (22%) | 0        | 100         | 100 |
| 34  | AJ    | 79/127 (62%)  | 59 (75%)  | 20 (25%) | 0        | 100         | 100 |
| 35  | AK    | 85/130 (65%)  | 74 (87%)  | 11 (13%) | 0        | 100         | 100 |
| 36  | AL    | 50/81 (62%)   | 39 (78%)  | 11 (22%) | 0        | 100         | 100 |
| 37  | AM    | 80/151 (53%)  | 71 (89%)  | 9 (11%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed       | Favoured  | Allowed   | Outliers | Percentiles |     |
|-----|-------|----------------|-----------|-----------|----------|-------------|-----|
| 38  | AN    | 78/188 (42%)   | 70 (90%)  | 8 (10%)   | 0        | 100         | 100 |
| 39  | AO    | 450/491 (92%)  | 387 (86%) | 63 (14%)  | 0        | 100         | 100 |
| 40  | AP    | 667/669 (100%) | 531 (80%) | 133 (20%) | 3 (0%)   | 30          | 64  |
| 41  | AQ    | 364/521 (70%)  | 312 (86%) | 51 (14%)  | 1 (0%)   | 36          | 69  |
| 42  | AR    | 27/29 (93%)    | 21 (78%)  | 6 (22%)   | 0        | 100         | 100 |
| 45  | Bb    | 271/556 (49%)  | 218 (80%) | 52 (19%)  | 1 (0%)   | 30          | 64  |
| 46  | Bf    | 134/148 (90%)  | 122 (91%) | 12 (9%)   | 0        | 100         | 100 |
| 47  | Bh    | 121/430 (28%)  | 100 (83%) | 21 (17%)  | 0        | 100         | 100 |
| 48  | Bi    | 99/241 (41%)   | 76 (77%)  | 23 (23%)  | 0        | 100         | 100 |
| 49  | Bl    | 89/154 (58%)   | 53 (60%)  | 35 (39%)  | 1 (1%)   | 11          | 43  |
| 50  | Bm    | 94/164 (57%)   | 63 (67%)  | 30 (32%)  | 1 (1%)   | 11          | 43  |
| 51  | Br    | 81/212 (38%)   | 64 (79%)  | 12 (15%)  | 5 (6%)   | 1           | 15  |
| 52  | Bw    | 331/480 (69%)  | 234 (71%) | 94 (28%)  | 3 (1%)   | 14          | 47  |
| 53  | Bx    | 77/102 (76%)   | 61 (79%)  | 16 (21%)  | 0        | 100         | 100 |
| 54  | Bz    | 121/419 (29%)  | 110 (91%) | 11 (9%)   | 0        | 100         | 100 |
| 55  | BA    | 36/91 (40%)    | 28 (78%)  | 8 (22%)   | 0        | 100         | 100 |
| 56  | Bt    | 27/98 (28%)    | 22 (82%)  | 5 (18%)   | 0        | 100         | 100 |
| 57  | BG    | 362/576 (63%)  | 309 (85%) | 46 (13%)  | 7 (2%)   | 6           | 33  |
| 58  | BP    | 83/91 (91%)    | 81 (98%)  | 2 (2%)    | 0        | 100         | 100 |
| 59  | BF    | 121/123 (98%)  | 98 (81%)  | 23 (19%)  | 0        | 100         | 100 |
| 60  | Ba    | 193/219 (88%)  | 146 (76%) | 47 (24%)  | 0        | 100         | 100 |
| 61  | Bc    | 323/362 (89%)  | 255 (79%) | 66 (20%)  | 2 (1%)   | 21          | 55  |
| 62  | Bd    | 214/515 (42%)  | 170 (79%) | 44 (21%)  | 0        | 100         | 100 |
| 63  | Be    | 97/139 (70%)   | 72 (74%)  | 25 (26%)  | 0        | 100         | 100 |
| 64  | Bg    | 126/129 (98%)  | 101 (80%) | 25 (20%)  | 0        | 100         | 100 |
| 65  | Bj    | 121/314 (38%)  | 97 (80%)  | 24 (20%)  | 0        | 100         | 100 |
| 66  | Bn    | 98/419 (23%)   | 86 (88%)  | 12 (12%)  | 0        | 100         | 100 |
| 67  | Bo    | 97/135 (72%)   | 75 (77%)  | 22 (23%)  | 0        | 100         | 100 |
| 68  | Bp    | 76/116 (66%)   | 59 (78%)  | 17 (22%)  | 0        | 100         | 100 |
| 69  | Bq    | 60/261 (23%)   | 51 (85%)  | 9 (15%)   | 0        | 100         | 100 |
| 70  | Bs    | 64/101 (63%)   | 53 (83%)  | 11 (17%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed          | Favoured   | Allowed    | Outliers | Percentiles |     |
|-----|-------|-------------------|------------|------------|----------|-------------|-----|
| 71  | Bu    | 96/195 (49%)      | 78 (81%)   | 18 (19%)   | 0        | 100         | 100 |
| 72  | Bv    | 147/195 (75%)     | 119 (81%)  | 28 (19%)   | 0        | 100         | 100 |
| 73  | By    | 74/142 (52%)      | 62 (84%)   | 12 (16%)   | 0        | 100         | 100 |
| 74  | BB    | 21/137 (15%)      | 20 (95%)   | 1 (5%)     | 0        | 100         | 100 |
| 75  | BC    | 66/112 (59%)      | 53 (80%)   | 13 (20%)   | 0        | 100         | 100 |
| 76  | BD    | 208/420 (50%)     | 164 (79%)  | 43 (21%)   | 1 (0%)   | 24          | 59  |
| 77  | BE    | 346/409 (85%)     | 277 (80%)  | 69 (20%)   | 0        | 100         | 100 |
| 78  | BI    | 264/266 (99%)     | 227 (86%)  | 37 (14%)   | 0        | 100         | 100 |
| 79  | BJ    | 347/349 (99%)     | 301 (87%)  | 46 (13%)   | 0        | 100         | 100 |
| 80  | BH    | 204/390 (52%)     | 176 (86%)  | 24 (12%)   | 4 (2%)   | 6           | 33  |
| 81  | BN    | 67/69 (97%)       | 57 (85%)   | 10 (15%)   | 0        | 100         | 100 |
| 82  | BM    | 77/79 (98%)       | 67 (87%)   | 10 (13%)   | 0        | 100         | 100 |
| 83  | BO    | 28/30 (93%)       | 28 (100%)  | 0          | 0        | 100         | 100 |
| 84  | BL    | 62/64 (97%)       | 56 (90%)   | 6 (10%)    | 0        | 100         | 100 |
| 86  | Az    | 80/109 (73%)      | 73 (91%)   | 6 (8%)     | 1 (1%)   | 9           | 40  |
| 87  | Ah    | 135/171 (79%)     | 126 (93%)  | 7 (5%)     | 2 (2%)   | 8           | 37  |
| 88  | BK    | 314/316 (99%)     | 289 (92%)  | 23 (7%)    | 2 (1%)   | 21          | 55  |
| 89  | Bk    | 119/125 (95%)     | 114 (96%)  | 4 (3%)     | 1 (1%)   | 16          | 50  |
| All | All   | 11835/18772 (63%) | 9765 (82%) | 2029 (17%) | 41 (0%)  | 37          | 69  |

5 of 41 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 57  | BG    | 89  | VAL  |
| 57  | BG    | 277 | SER  |
| 57  | BG    | 278 | PRO  |
| 87  | Ah    | 91  | PRO  |
| 1   | Aa    | 81  | LYS  |

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

| Mol | Chain | Analysed      | Rotameric  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 1   | Aa    | 82/284 (29%)  | 81 (99%)   | 1 (1%)   | 63          | 72  |
| 2   | Ab    | 121/169 (72%) | 121 (100%) | 0        | 100         | 100 |
| 3   | Ac    | 174/267 (65%) | 173 (99%)  | 1 (1%)   | 78          | 80  |
| 4   | AD    | 54/158 (34%)  | 54 (100%)  | 0        | 100         | 100 |
| 5   | Ad    | 181/260 (70%) | 181 (100%) | 0        | 100         | 100 |
| 6   | Ae    | 133/168 (79%) | 130 (98%)  | 3 (2%)   | 44          | 64  |
| 7   | Af    | 84/86 (98%)   | 84 (100%)  | 0        | 100         | 100 |
| 8   | Ag    | 43/196 (22%)  | 43 (100%)  | 0        | 100         | 100 |
| 9   | Ai    | 116/128 (91%) | 116 (100%) | 0        | 100         | 100 |
| 10  | Aj    | 135/170 (79%) | 133 (98%)  | 2 (2%)   | 57          | 69  |
| 11  | Ak    | 103/138 (75%) | 102 (99%)  | 1 (1%)   | 68          | 75  |
| 12  | Al    | 147/236 (62%) | 147 (100%) | 0        | 100         | 100 |
| 13  | Am    | 111/146 (76%) | 109 (98%)  | 2 (2%)   | 51          | 67  |
| 14  | An    | 119/137 (87%) | 118 (99%)  | 1 (1%)   | 73          | 77  |
| 15  | Ao    | 91/98 (93%)   | 89 (98%)   | 2 (2%)   | 45          | 64  |
| 16  | Ap    | 103/199 (52%) | 99 (96%)   | 4 (4%)   | 28          | 52  |
| 17  | Aq    | 93/110 (84%)  | 93 (100%)  | 0        | 100         | 100 |
| 18  | Ar    | 122/244 (50%) | 121 (99%)  | 1 (1%)   | 73          | 77  |
| 19  | As    | 98/233 (42%)  | 98 (100%)  | 0        | 100         | 100 |
| 20  | At    | 92/146 (63%)  | 91 (99%)   | 1 (1%)   | 65          | 73  |
| 21  | Au    | 121/132 (92%) | 117 (97%)  | 4 (3%)   | 33          | 56  |
| 22  | Av    | 175/216 (81%) | 172 (98%)  | 3 (2%)   | 53          | 68  |
| 23  | Aw    | 64/126 (51%)  | 62 (97%)   | 2 (3%)   | 35          | 57  |
| 24  | Ax    | 83/173 (48%)  | 81 (98%)   | 2 (2%)   | 43          | 63  |
| 25  | Ay    | 105/127 (83%) | 105 (100%) | 0        | 100         | 100 |
| 26  | AA    | 28/65 (43%)   | 28 (100%)  | 0        | 100         | 100 |
| 27  | AB    | 36/116 (31%)  | 36 (100%)  | 0        | 100         | 100 |
| 28  | AC    | 46/52 (88%)   | 46 (100%)  | 0        | 100         | 100 |
| 29  | AE    | 35/87 (40%)   | 35 (100%)  | 0        | 100         | 100 |
| 30  | AF    | 70/206 (34%)  | 69 (99%)   | 1 (1%)   | 59          | 70  |
| 31  | AG    | 55/82 (67%)   | 55 (100%)  | 0        | 100         | 100 |

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| Mol | Chain | Analysed      | Rotameric  | Outliers | Percentiles |     |
|-----|-------|---------------|------------|----------|-------------|-----|
| 32  | AH    | 98/130 (75%)  | 98 (100%)  | 0        | 100         | 100 |
| 33  | AI    | 185/209 (88%) | 184 (100%) | 1 (0%)   | 81          | 82  |
| 34  | AJ    | 71/111 (64%)  | 71 (100%)  | 0        | 100         | 100 |
| 35  | AK    | 76/109 (70%)  | 76 (100%)  | 0        | 100         | 100 |
| 36  | AL    | 42/63 (67%)   | 42 (100%)  | 0        | 100         | 100 |
| 37  | AM    | 73/130 (56%)  | 73 (100%)  | 0        | 100         | 100 |
| 38  | AN    | 69/163 (42%)  | 69 (100%)  | 0        | 100         | 100 |
| 39  | AO    | 388/424 (92%) | 388 (100%) | 0        | 100         | 100 |
| 41  | AQ    | 311/461 (68%) | 311 (100%) | 0        | 100         | 100 |
| 45  | Bb    | 243/495 (49%) | 241 (99%)  | 2 (1%)   | 73          | 77  |
| 46  | Bf    | 116/125 (93%) | 115 (99%)  | 1 (1%)   | 70          | 75  |
| 47  | Bh    | 99/360 (28%)  | 99 (100%)  | 0        | 100         | 100 |
| 48  | Bi    | 94/211 (44%)  | 94 (100%)  | 0        | 100         | 100 |
| 49  | Bl    | 78/129 (60%)  | 78 (100%)  | 0        | 100         | 100 |
| 50  | Bm    | 84/144 (58%)  | 84 (100%)  | 0        | 100         | 100 |
| 51  | Br    | 73/180 (41%)  | 64 (88%)   | 9 (12%)  | 4           | 20  |
| 52  | Bw    | 289/404 (72%) | 288 (100%) | 1 (0%)   | 86          | 85  |
| 53  | Bx    | 68/85 (80%)   | 66 (97%)   | 2 (3%)   | 37          | 58  |
| 54  | Bz    | 107/368 (29%) | 105 (98%)  | 2 (2%)   | 50          | 66  |
| 55  | BA    | 35/81 (43%)   | 35 (100%)  | 0        | 100         | 100 |
| 56  | Bt    | 25/81 (31%)   | 25 (100%)  | 0        | 100         | 100 |
| 60  | Ba    | 173/191 (91%) | 172 (99%)  | 1 (1%)   | 78          | 80  |
| 61  | Bc    | 310/343 (90%) | 308 (99%)  | 2 (1%)   | 78          | 80  |
| 62  | Bd    | 185/463 (40%) | 185 (100%) | 0        | 100         | 100 |
| 63  | Be    | 90/126 (71%)  | 90 (100%)  | 0        | 100         | 100 |
| 64  | Bg    | 112/113 (99%) | 110 (98%)  | 2 (2%)   | 51          | 67  |
| 65  | Bj    | 103/264 (39%) | 102 (99%)  | 1 (1%)   | 68          | 75  |
| 66  | Bn    | 94/378 (25%)  | 94 (100%)  | 0        | 100         | 100 |
| 67  | Bo    | 82/113 (73%)  | 82 (100%)  | 0        | 100         | 100 |
| 68  | Bp    | 71/99 (72%)   | 71 (100%)  | 0        | 100         | 100 |
| 69  | Bq    | 51/224 (23%)  | 50 (98%)   | 1 (2%)   | 48          | 65  |

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| Mol | Chain | Analysed         | Rotameric  | Outliers | Percentiles |     |
|-----|-------|------------------|------------|----------|-------------|-----|
| 70  | Bs    | 61/92 (66%)      | 61 (100%)  | 0        | 100         | 100 |
| 71  | Bu    | 86/170 (51%)     | 85 (99%)   | 1 (1%)   | 63          | 72  |
| 72  | Bv    | 132/173 (76%)    | 132 (100%) | 0        | 100         | 100 |
| 73  | By    | 61/115 (53%)     | 61 (100%)  | 0        | 100         | 100 |
| 74  | BB    | 22/127 (17%)     | 22 (100%)  | 0        | 100         | 100 |
| 75  | BC    | 58/94 (62%)      | 57 (98%)   | 1 (2%)   | 53          | 68  |
| 76  | BD    | 188/368 (51%)    | 188 (100%) | 0        | 100         | 100 |
| 77  | BE    | 296/351 (84%)    | 296 (100%) | 0        | 100         | 100 |
| 86  | Az    | 73/96 (76%)      | 64 (88%)   | 9 (12%)  | 4           | 20  |
| 87  | Ah    | 119/144 (83%)    | 114 (96%)  | 5 (4%)   | 26          | 50  |
| 89  | Bk    | 104/108 (96%)    | 96 (92%)   | 8 (8%)   | 12          | 37  |
| All | All   | 8115/13570 (60%) | 8035 (99%) | 80 (1%)  | 65          | 75  |

5 of 80 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 75  | BC    | 42  | ILE  |
| 87  | Ah    | 129 | ILE  |
| 86  | Az    | 21  | ILE  |
| 86  | Az    | 77  | TYR  |
| 89  | Bk    | 55  | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 60  | Ba    | 25  | HIS  |
| 66  | Bn    | 364 | HIS  |
| 60  | Ba    | 95  | ASN  |
| 61  | Bc    | 338 | HIS  |
| 70  | Bs    | 62  | HIS  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 43  | 1     | 2836/2842 (99%) | 1125 (39%)        | 66 (2%)         |
| 44  | 3     | 118/118 (100%)  | 49 (41%)          | 7 (5%)          |

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| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 85  | 2     | 1737/1743 (99%) | 762 (43%)         | 65 (3%)         |
| All | All   | 4691/4703 (99%) | 1936 (41%)        | 138 (2%)        |

5 of 1936 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 43  | 1     | 17  | A    |
| 43  | 1     | 27  | A    |
| 43  | 1     | 37  | G    |
| 43  | 1     | 38  | G    |
| 43  | 1     | 45  | A    |

5 of 138 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 85  | 2     | 1459 | A    |
| 85  | 2     | 1484 | G    |
| 85  | 2     | 1796 | U    |
| 43  | 1     | 2051 | U    |
| 43  | 1     | 2050 | A    |

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 85  | 2     | 39               |
| 43  | 1     | 5                |
| 58  | BP    | 3                |
| 45  | Bb    | 1                |

The worst 5 of 48 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1     | 2     | 120:C     | O3'    | 128:C     | P      | 28.73        |
| 1     | BP    | 204:ALA   | C      | 205:ALA   | N      | 21.29        |
| 1     | 2     | 1193:G    | O3'    | 1202:C    | P      | 17.46        |
| 1     | 2     | 1220:G    | O3'    | 1368:C    | P      | 17.36        |
| 1     | 2     | 98:G      | O3'    | 111:C     | P      | 17.08        |

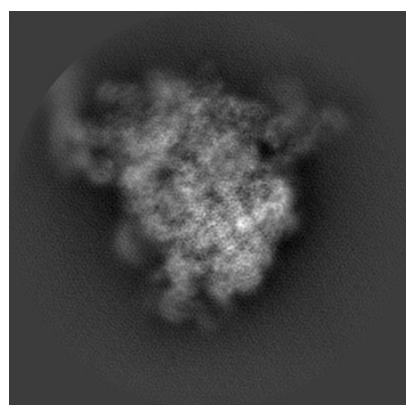
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10654. These allow visual inspection of the internal detail of the map and identification of artifacts.

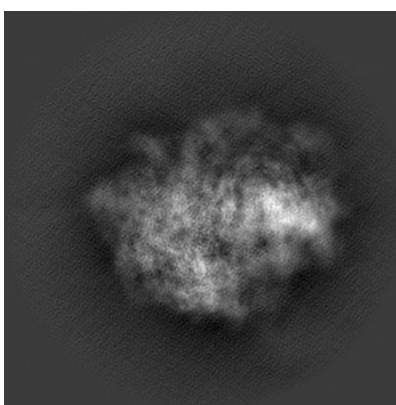
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

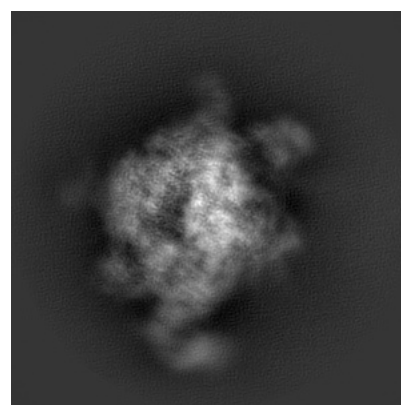
#### 6.1.1 Primary map



X



Y

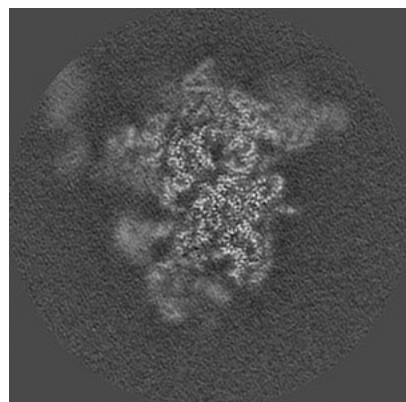


Z

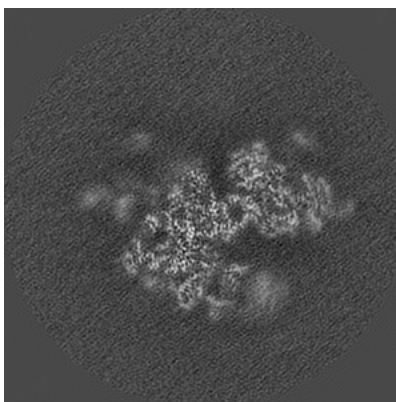
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

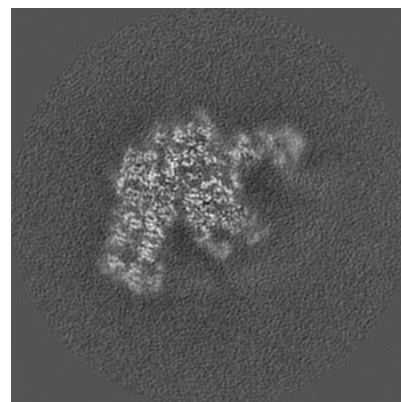
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

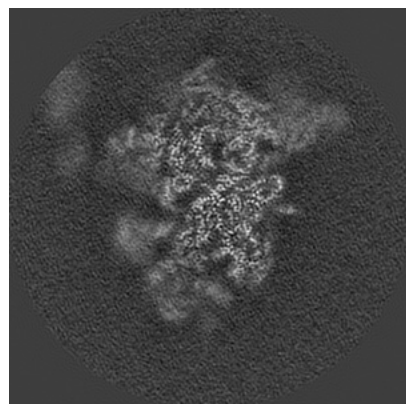


Z Index: 200

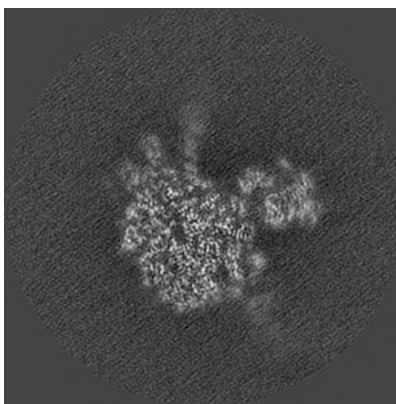
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

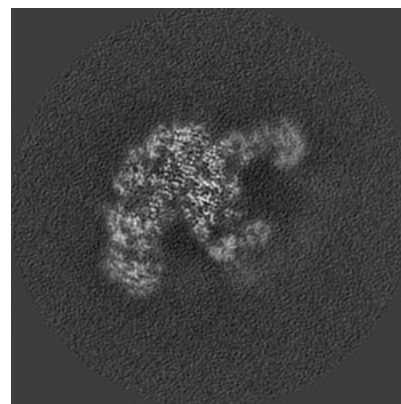
### 6.3.1 Primary map



X Index: 201



Y Index: 229

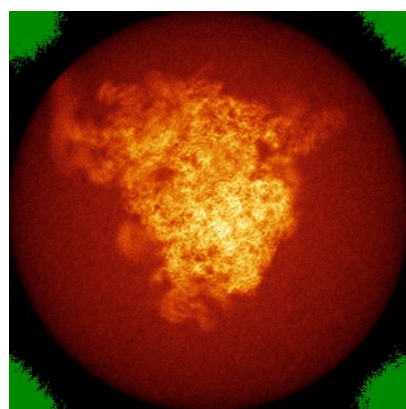


Z Index: 205

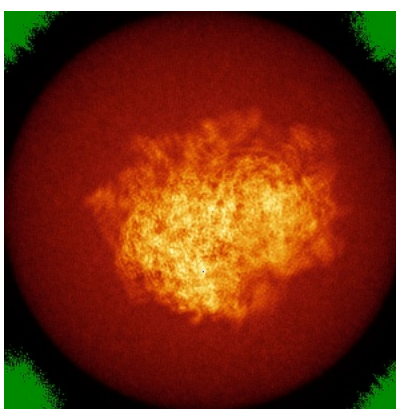
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

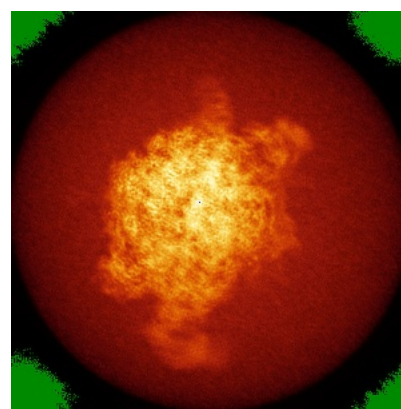
### 6.4.1 Primary map



X



Y

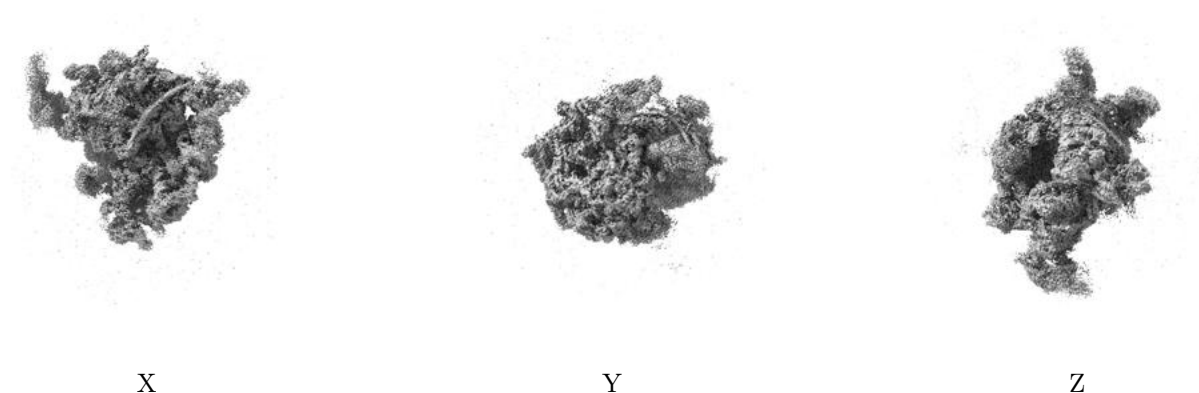


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.035. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

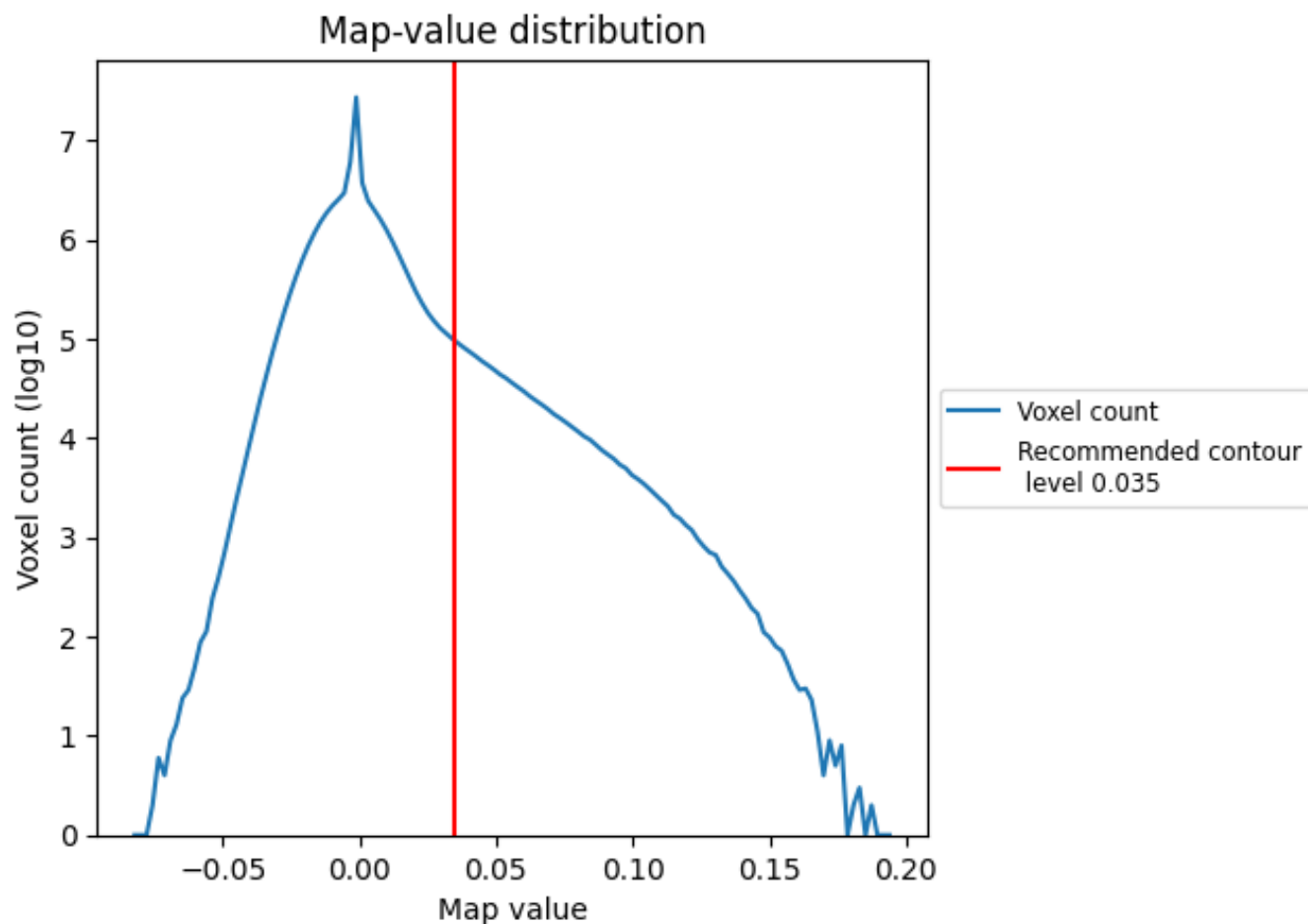
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

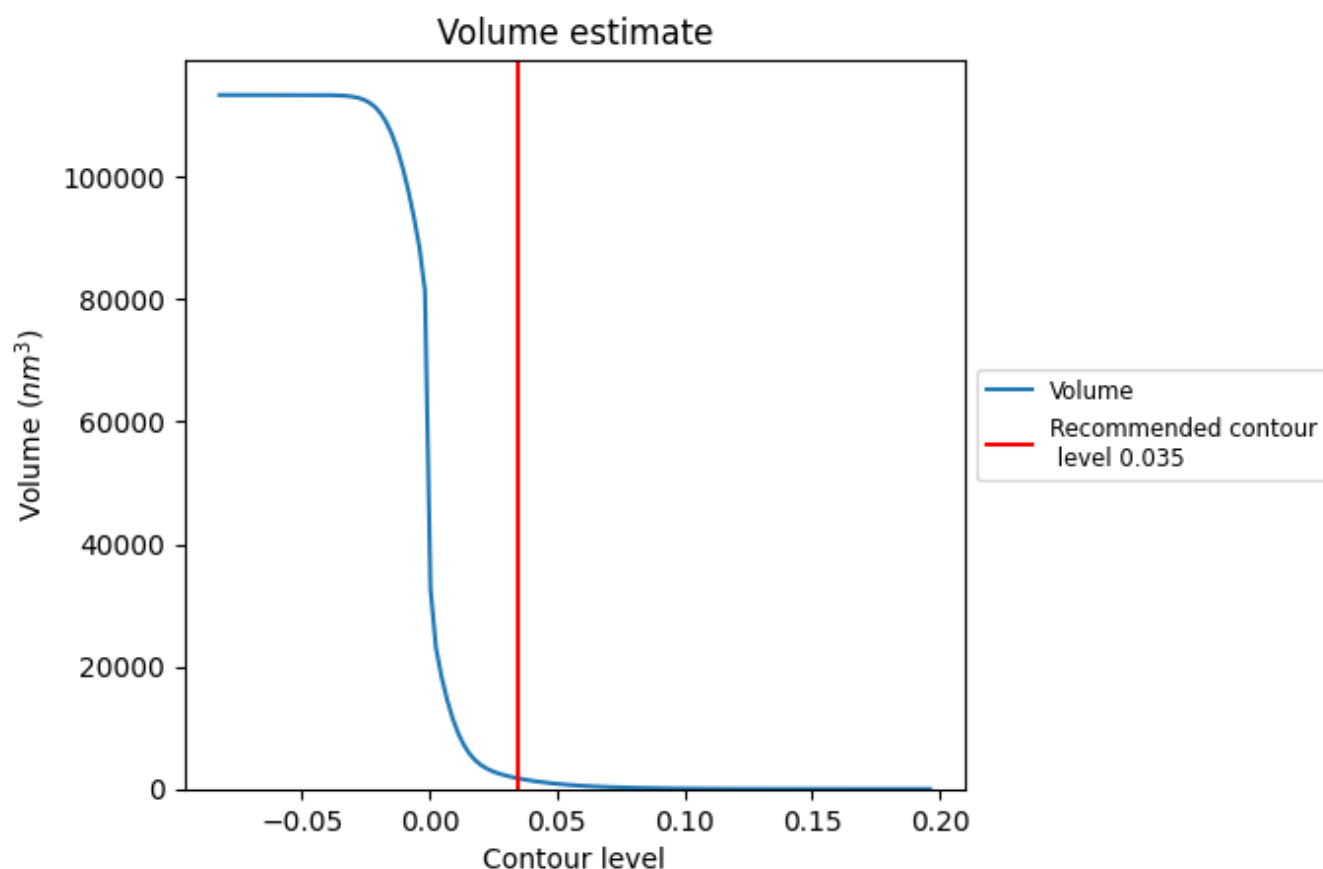
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

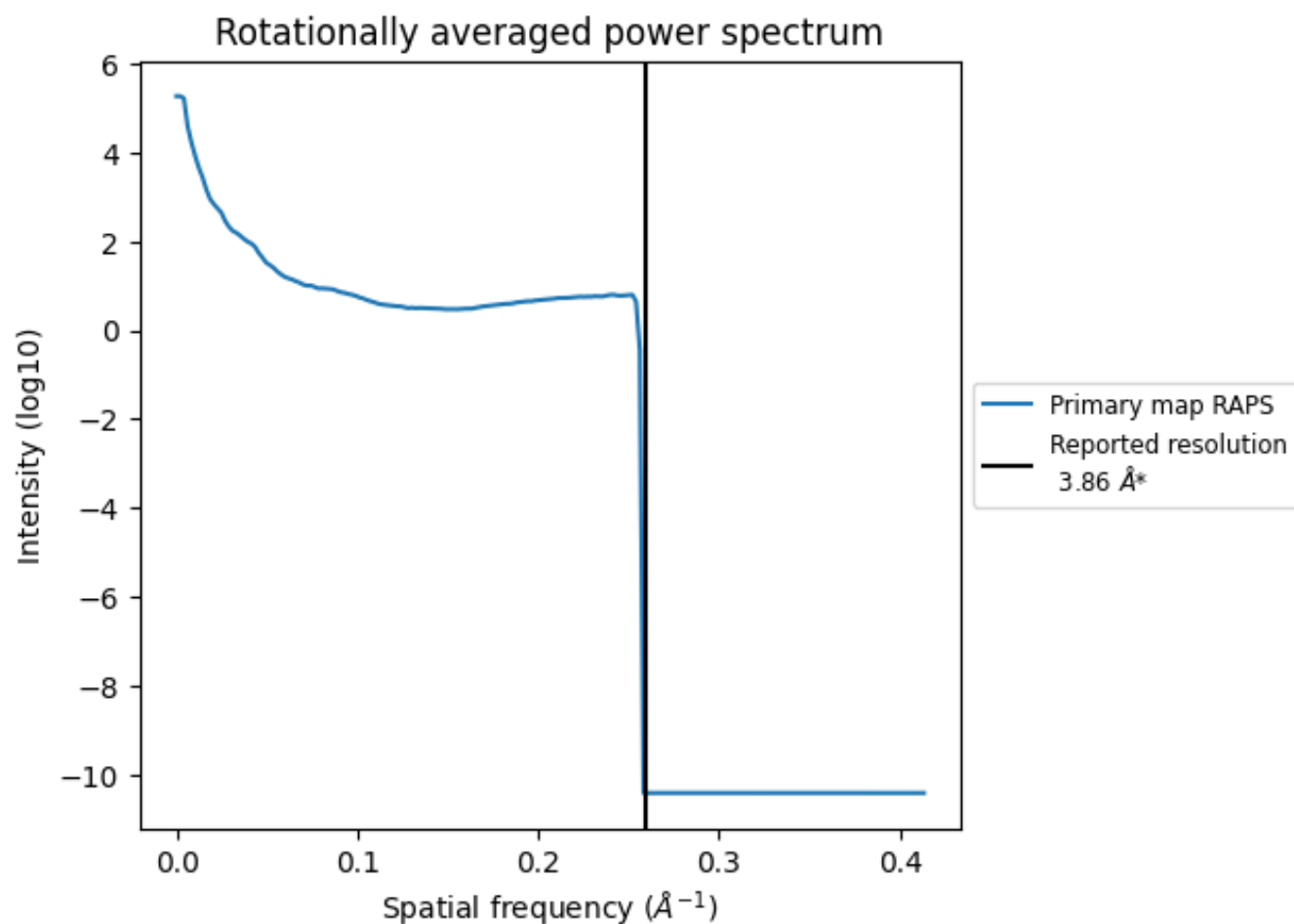
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1711  $\text{nm}^3$ ; this corresponds to an approximate mass of 1546 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.259 Å<sup>-1</sup>

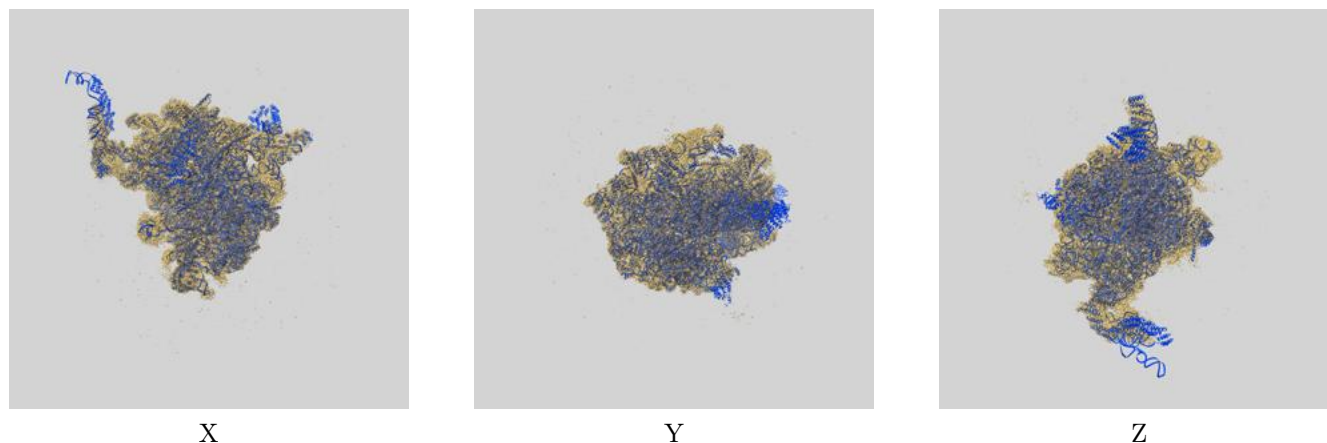
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

## 9 Map-model fit [i](#)

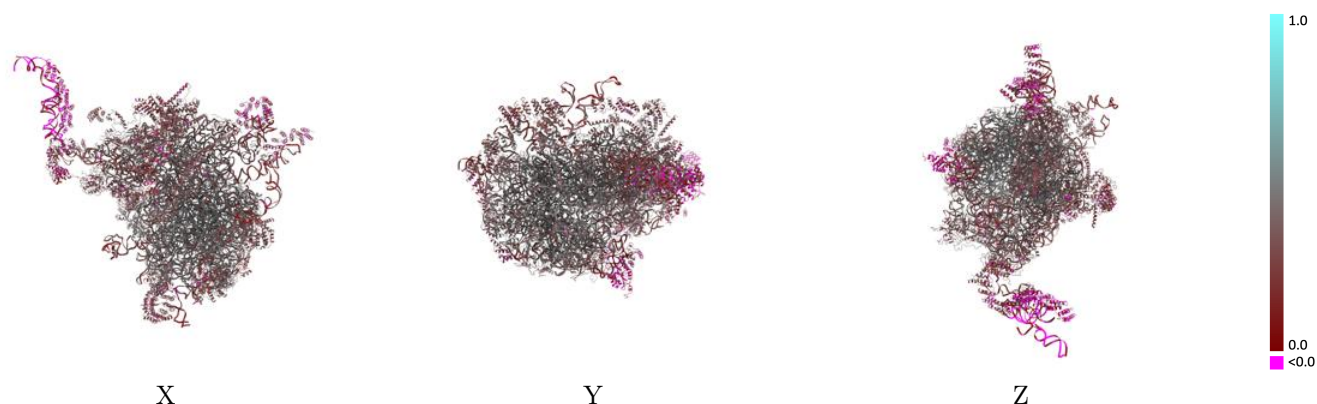
This section contains information regarding the fit between EMDB map EMD-10654 and PDB model 6XYW. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

### 9.1 Map-model overlay [i](#)



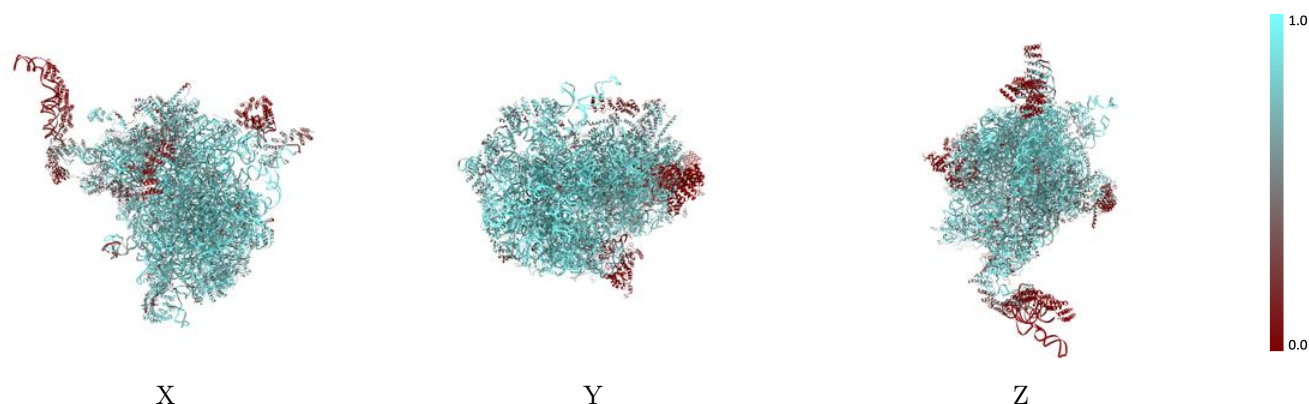
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



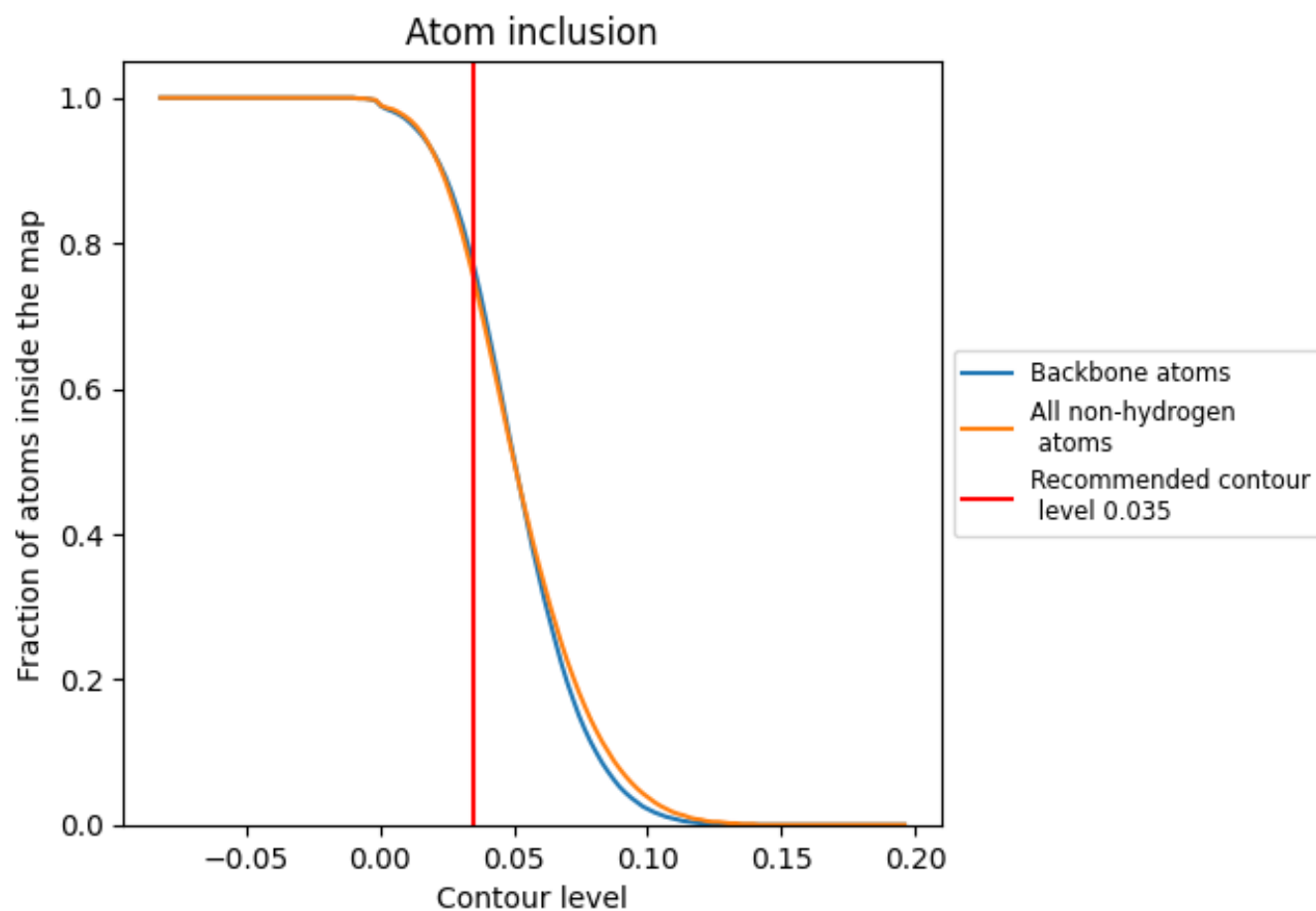
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.035).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.035) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion                                                                             | Q-score                                                                                     |
|-------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------|
| All   |  0.7510   |  0.3590    |
| 1     |  0.8950   |  0.3950    |
| 2     |  0.8180   |  0.3350    |
| 3     |  0.9540   |  0.3880    |
| AA    |  0.7600   |  0.3460    |
| AB    |  0.8160   |  0.4630    |
| AC    |  0.8330   |  0.4390    |
| AD    |  0.8080   |  0.4600    |
| AE    |  0.6680   |  0.4590    |
| AF    |  0.7150   |  0.3070    |
| AG    |  0.7700   |  0.4460    |
| AH    |  0.8200   |  0.4400    |
| AI    |  0.6970   |  0.3330    |
| AJ    |  0.0550   |  0.1150    |
| AK    |  0.7830  |  0.4140   |
| AL    |  0.8420 |  0.4370  |
| AM    |  0.7880 |  0.4290  |
| AN    |  0.7230 |  0.4140  |
| AO    |  0.7120 |  0.3420  |
| AP    |  0.6910 |  0.2700  |
| AQ    |  0.6640 |  0.3290  |
| AR    |  0.9030 |  0.3810  |
| Aa    |  0.7230 |  0.4570  |
| Ab    |  0.7970 |  0.4760  |
| Ac    |  0.8150 |  0.4450  |
| Ad    |  0.7900 |  0.4370  |
| Ae    |  0.6480 |  0.3580  |
| Af    |  0.3760 |  0.3710  |
| Ag    |  0.7510 |  0.4030  |
| Ah    |  0.0080 |  -0.0030 |
| Ai    |  0.1070 |  0.1780  |
| Aj    |  0.8210 |  0.4370  |
| Ak    |  0.6510 |  0.4550  |
| Al    |  0.7710 |  0.4360  |
| Am    |  0.5370 |  0.4340  |



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| Chain | Atom inclusion                                                                             | Q-score                                                                                    |
|-------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|
| An    |  0.8230   |  0.4470   |
| Ao    |  0.8350   |  0.4090   |
| Ap    |  0.7600   |  0.4430   |
| Aq    |  0.8180   |  0.4250   |
| Ar    |  0.8070   |  0.4250   |
| As    |  0.7920   |  0.4550   |
| At    |  0.7480   |  0.4530   |
| Au    |  0.7810   |  0.3890   |
| Av    |  0.6890   |  0.3670   |
| Aw    |  0.8370   |  0.4560   |
| Ax    |  0.7880   |  0.4540   |
| Ay    |  0.7520   |  0.3860   |
| Az    |  0.7420   |  0.3300   |
| BA    |  0.2150   |  0.2410   |
| BB    |  0.5100   |  0.4510   |
| BC    |  0.6500   |  0.3240   |
| BD    |  0.6820   |  0.3430   |
| BE    |  0.5400   |  0.3120   |
| BF    |  0.6710   |  0.3470   |
| BG    |  0.3520  |  0.2080  |
| BH    |  0.0540 |  0.2250 |
| BI    |  0.4170 |  0.2170 |
| BJ    |  0.0160 |  0.1570 |
| BK    |  0.0230 |  0.0260 |
| BL    |  0.5840 |  0.2630 |
| BM    |  0.6560 |  0.3030 |
| BN    |  0.7940 |  0.3430 |
| BO    |  0.7870 |  0.3040 |
| BP    |  0.7630 |  0.2640 |
| Ba    |  0.5290 |  0.3400 |
| Bb    |  0.6210 |  0.3850 |
| Bc    |  0.6580 |  0.3540 |
| Bd    |  0.6630 |  0.4100 |
| Be    |  0.6500 |  0.3760 |
| Bf    |  0.4270 |  0.3190 |
| Bg    |  0.6420 |  0.4110 |
| Bh    |  0.6490 |  0.3370 |
| Bi    |  0.6690 |  0.3420 |
| Bj    |  0.6290 |  0.3770 |
| Bk    |  0.5830 |  0.3110 |
| Bl    |  0.5260 |  0.3330 |
| Bm    |  0.7070 |  0.4040 |

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| Chain | Atom inclusion                                                                           | Q-score                                                                                  |
|-------|------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------|
| Bn    |  0.7270 |  0.3950 |
| Bo    |  0.7430 |  0.4110 |
| Bp    |  0.7440 |  0.4300 |
| Bq    |  0.6130 |  0.3900 |
| Br    |  0.3840 |  0.0570 |
| Bs    |  0.5450 |  0.3960 |
| Bt    |  0.7590 |  0.4240 |
| Bu    |  0.4110 |  0.3400 |
| Bv    |  0.6360 |  0.3060 |
| Bw    |  0.5520 |  0.3120 |
| Bx    |  0.5350 |  0.3790 |
| By    |  0.6640 |  0.3250 |
| Bz    |  0.5720 |  0.3380 |